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**Miki**

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(54) **ANTI-HUMAN NOROVIRUS GII ANTIBODY**

(75) Inventor: Motohiro Miki, Gosen (JP)

(73) Assignee: DENKA SEIKEN CO., LTD., Tokyo (JP)

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G01N 33/569 (2006.01)(52) **U.S. Cl.**

CPC ..... G01N 33/5693 (2013.01); C07K 16/10 (2013.01); C07K 2317/34 (2013.01); C07K 2317/55 (2013.01); G01N 2333/08 (2013.01)

(58) **Field of Classification Search**

CPC ..... A61K 39/12; C07K 2317/55; C07K 7/06; C07K 14/08

See application file for complete search history.

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**Primary Examiner — Bao Li**(74) **Attorney, Agent, or Firm — Oblon, McClelland, Maier & Neustadt, L.L.P.**(57) **ABSTRACT**

An anti-human-norovirus GII antibody which responds to substantially all genotypes of the human noroviruses belonging to GII and which can comprehensively detect such human noroviruses GII. The anti-human-norovirus GII antibody that binds to at least one of epitopes which are contained in amino acid regions represented by the following formulas (1) and (2):

P-X<sup>1</sup>-X<sup>2</sup>-P-G-E

(1) (SEQ ID NO: 2)

X<sup>3</sup>-X<sup>4</sup>-X<sup>5</sup>-F-Y-X<sup>6</sup>-L-X<sup>7</sup>-P-X<sup>8</sup>

(2) (SEQ ID NO: 3)

(wherein, X<sup>1</sup> represents L, V, N, T, S, M, or R; X<sup>2</sup> represents F, Y, or M; X<sup>3</sup> represents V or G; X<sup>4</sup> represents N or S; X<sup>5</sup> represents Q, P, or S; X<sup>6</sup> represents S, T, or I; X<sup>7</sup> represents A or S; and X<sup>8</sup> represents M or V), and of an epitope formed of amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or an epitope formed of an amino acid corresponding to amino acid 483, the regions and the amino acids being present in the P domain of a capsid structural protein of a human norovirus GII.

(56)

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Fig. 1-1

Fig. 1-2

485 (G2/1)  
 NG1 (G2/2)  
 MK04 (G2/2)  
 336 (G2/3)  
 18-3 (G2/3)  
 809  
 104 (G2/4)  
 2006a (Aomori) (G2/4)  
 2006b (Saga) (G2/4)  
 2007a (G2/4)  
 2008a (Apeidoorn\_317\_NL\_2007)  
 2008a (MiyoshiG2-4)  
 2009a (New)  
 754 (G2/5)  
 445 (G2/6)  
 7x (G2/6)  
 U25 (G2/8)  
 V1et026 (G2/10)  
 76 (G2/12)  
 47 (G2/14)  
 Kamo8 (G2/15)  
 Alpha23 (G2/17)

61 : NGEFTVSPRNSPGEILLNLELPNELPNFLAHLSRMYNGYAGGVEQVLLAGNAFTACKLV 120  
 61 : NGEFTVSPRNSPGEVLLSLELPNELPNPLAHLARMYNGYAGGMEQVMLAGNAFTACKLV 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLARMYNGYAGGMEQVMLAGNAFTACKLV 120  
 61 : GGEFTVSPRNSPGEVLLNLELPPEINPYLAHLARMYNGYAGGFEVQVVLAGNAFTACKV1 120  
 61 : QGEFTVSPRNSPGEMLNLELPNELPNPLSHELMQVQVVLAGNAFTACKV1 120  
 61 : QGEFTVSPRNSPGEMLNLELPNELPNPLSHELMQVQVVLAGNAFTACKV1 120  
 61 : QGEFTVSPRNSPGEMLNLELPNELPNPLSHELMQVQVVLAGNAFTACKV1 120  
 61 : QGEFTVSPRNSPGEMLNLELPNELPNPLSHELMQVQVVLAGNAFTACKV1 120  
 61 : AGEFTVSPRNSPGEFLDLELPNELPNPLAHLARMYNGHAGGMEQIVLAGNAFTACKV1 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLSRMYNGYAGGMEQVIMLAGNAFTACKV1 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLSRMYNGYAGGVEQVLLAGNAFTACKLV 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLSRMYNGYAGGVEQVLLAGNAFTACKV1 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLSRMYNGYAGGVEQVLLAGNAFTACKLV 120  
 61 : NGEFTVSPRNSPGEVLLNLELPNELPNPLAHLSRMYNGYAGGVEQVLLAGNAFTACKLV 120

Fig. 1-3

Fig. 1-4

485 (G2/1)  
 NG1 (G2/2)  
 MK04 (G2/2)  
 336 (G2/3)  
 18-3 (G2/3)  
 809  
 104 (G2/4)  
 2006a (Aomori) (G2/4)  
 2006b (Saga) (G2/4)  
 2007a (G2/4)  
 2008a (Apedooron\_317\_NL\_2007)  
 2008a (Miyoshi) G2-4)  
 2009a (New)  
 754 (G2/5)  
 445 (G2/6)  
 7k (G2/6)  
 U25 (G2/8)  
 V1et026 (G2/10)  
 76 (G2/12)  
 47 (G2/14)  
 Kanno 8 (G2/15)  
 Alpha 23 (G2/17)

181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDNLYPPTVESKTKPFTLPILTLGELNS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPFTLPILTGELNS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPFTLPILTGELNS 240  
 181 : MLYTPLRANSNGDDVFTVSCRVLTRPSPDFSFNFLVPPPTVESKTKPFTLPILTLGELNS 240  
 181 : MLYTPLRANSNGDDVFTVSCRVLTRPSPDFSFNFLVPPPTVESKTKLFTLPILTISEMNS 240  
 181 : MLYTPLRANSNGDDVFTVSCRVLTRPSPDFSFNFLVPPPTVESKTKPFTLPILTLGELNS 240  
 181 : MLYTPLRANSNGDDVFTVSCRVLTRPSPDFSFNFLVPPPTVESRTRKPFTVPILTVEEMNS 240  
 181 : MLYTPLRANSAGDDVFTVSCRVLTRPSPDFDFIFLVPPPTVESRTRKPFTVPILTVEEMNS 240  
 181 : MLYTPLRANSAGDDVFTVSCRVLTRPSPDFDFIFLVPPPTVESRTRKPFTVPILTVEEMNS 240  
 181 : MLYTPLRANNAGEDDVFTVSCRVLTRPSPDFDFIFLVPPPTVESRTRKPFTVPILTVEEMNS 240  
 181 : MLYTPLRRA-NSGEDDVFTVSCRVLTRPAPDFEFTFLVPPPTVESKTKPFTLPILTLGELNS 239  
 181 : MLYTPLRA-NSGEDDVFTVSCRVLTRPAPDFEFTFLVPPPTVESKTKPFTLPILTLGELNS 239  
 181 : MLYTPLRANNAGEDDVFTVSCRVLTRPSPDFDNLYPPTVESKTKAFTLPILKISEMNTS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPFTLPILTGELTS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDNLYVPPTLESKTKPFTLPILTLGELTS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDNLYVPPTLESKTKPFTLPILTLGELTS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDNLYVPPPTVESKTKPFTLPILTLGELTS 240  
 181 : MLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDNLYVPPPTVESKTKPFTLPILTLGELTS 240  
 181 : WLYTPLRTNGSGDDDSFTVSGRLTRPSQDFEAFLIPPTVETKTTPFVPGFSVQEMSNS 240

Fig. 1-5

4 8 5 (G2/1) 24 1 : RFPAPIDELYTSPNEGGLVQQPQNNGRSTLDGEELLLGTTQLVPSNICSLRGRI-----  
 NG 1 (G2/2) 24 1 : RFPVSDQMYTSPNEVISVQCQNGRCTLTDGEELQGTTQLQVSGICAFKGEV-----  
 MK0 4 (G2/2) 24 1 : RFPVSDQMYTSPNEVISVQCQNGRCTLTDGEELQGTTQLQVSGICAFKGEV-----  
 3 3 6 (G2/3) 24 1 : RFPVPIDSLSLHTSPTESVVVQCCQNNGRVTLDGEELMGTTLPSQICAFRGTLTRPTNRA SDQ 300  
 18 - 3 (G2/3) 24 1 : RFPVPIDSLSLHTSPTENIVVQCQNGRVTLDGEELMGTTLPSQICAFRGTLTRPTNRA SDQ 300  
 8 0 9 24 1 : RFPVPIDESLHTSPTENIVVQCQNGRVTLDGEELMGTTLPSQICAFRGVLTRSTSRASDQ 300  
 10 4 (G2/4) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSAVNICTRFRGDV-----  
 2 0 0 6 a (Aomori) (G2/4) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSPVNICTRFRGDV-----  
 2 0 0 6 b (Saga) (G2/4) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSPVNICTRFRGDV-----  
 2 0 0 7 a (G2/4) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSAVNICTRFRGDV-----  
 2 0 0 8 a (Apeidoorn\_317\_NL\_2007) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSPVNICTRFRGDV-----  
 2 0 0 8 a (Miyoshi G2-4) 24 1 : RFPPIPLEKLYTGPPSSAFVVVQPPQNNGRCTTDGVULLGTTQLSPVNICTRFRGDV-----  
 2 0 0 9 a (New) 24 1 : RFPPIPLEKLYTGPPSSFTVVVQPPQNNGRCTTDGVULLGTTQLSPVNICTRFRGDV-----  
 7 5 4 (G2/5) 24 1 : RFPPLSIDEMVTSPNESIVVQQPQNNGRVTLDGEELLGITQLQACNICSI RGKV-----  
 4 4 5 (G2/6) 24 0 : RFPAAIDMLYADPNESIVVQQPQNNGRCTLTDGTLQGTTQLVPTQICAFRGTLISQTARATDS 299  
 7 k (G2/6) 24 0 : RFPAAIDMLYTDPNESIVVQQPQNNGRCTLTDGTLQGTTQLVPTQICAFRGTLISQTARAADS 299  
 U2 5 (G2/8) 24 1 : RFPPIPVDPQMYTSRNENIVVQQPQNNGRVTLDGEELQGTTQLQPVUSICGFRGTL-----  
 V i e t 0 2 6 (G2/10) 24 1 : RFPPLPIDVLYTNPNESAIVQCQNGRCTLTDGEELQGTTQLLPTGICAFRGKV-----  
 7 6 (G2/12) 24 1 : RFPVPIDELYTSPNESLVVQQPQNNGRCALDGEELQGTTQLLPTAICSFRRGI-----  
 4 7 (G2/14) 24 1 : RFPPIPEQLYTAPNETNVVQCCQNNGRCTLTDGEELQGTTQLLSSAVCFLQGR-----  
 Kamo 8 (G2/15) 24 1 : RFPVPIDAMYTSPNDSIVVQQPQNNGRATIDGEELLGTTLQLI PSGICSFRGKI-----  
 A1pha23 (G2/17) 24 1 : RWPAAISAMVVRGNEPPQQFQNNGRAHLDGMLLGTTPVSPNYIASYRGISTGN SRSASSE 300

Fig. 1-6

485 (G 2/1)  
 NG1 (G 2/2)  
 MK04 (G 2/2)  
 336 (G 2/3)  
 18-3 (G 2/3)  
 809  
 104 (G 2/4)  
 2006 a (Aomori) (G 2/4)  
 2006 b (Saga) (G 2/4)  
 2007 a (G 2/4)  
 2008 a (Apeidoorn\_317\_NL\_2007)  
 2008 a (Miyoshi G 2-4)  
 2009 a (New)  
 754 (G 2/5)  
 445 (G 2/6)  
 7k (G 2/6)  
 U25 (G 2/8)  
 Vier026 (G 2/10)  
 76 (G 2/12)  
 47 (G 2/14)  
 Kamo8 (G 2/15)  
 A1ph23 (G 2/17)

291 : NAHLPDNQH--RWNMQVTNANGTPFDPTEDVPAPLGTDFLANIYGVTQSQRN---PDNTC 345  
 291 : TAHLHDNDH--LYNVTITNLNGPFDPSEDIAPLGVPDFQGRVFGVISQRDKQNAAGHS 348  
 291 : TAHLHDNDH--LYNVTITNLNGSPFDPSEDIAPLGVPDFQGRVFGVISQRDKHNSPGHN 348  
 301 : ADTATPRLPNHQWHIQLDLNLngTPYDPAEDIAPLGTDFRGKVFVGVASQRD-PDGT--- 356  
 301 : ADTPTPRLPNHRWHIQLDLNLngTPYDPAEDIAPLGTDFRGKVFVGVASQRN-PDST--- 356  
 301 : ADTATPRLFNYYWHVQLDNLNGTPYDPAEDIAPGLGTPDFRGKVFVGVASQRN-LDST--- 356  
 291 : -THIAGSHD---YTMMNLASQNWSNNDPTEEIPAPLGTDPFVGKIQGMLTQ-----TTR 339  
 291 : -THIAGTQE---YTMMNLASQNWNNDPTEEIPAPLGTDPFVGKIQGVLTQ-----TTR 339  
 291 : -THIAGSRN---YTMMNLASLNWNNDPTEEIPAPLGTDPFVGKIQGLLTQ-----TTR 339  
 291 : -THIAGSRN---YTMMNLASQNWNNDPTEEIPAPLGTDPFVGKIQGMLTQ-----TTR 339  
 291 : -THITGSRN---YTMMNLATQNWNNDPTEEIPAPLGTDPFVGKIQGVLTQ-----TTR 339  
 291 : -AHIAGSRN---YTMMNLAPLNWNNDPTEEIPAPLCTDPFVGKIQGMLTQ-----TTR 339  
 291 : -THIAGSRN---YTMMNLASQNWNNDPTEEIPAPLGTDPFVGKIQGVLTQ-----TTR 339  
 291 : TCGQVPSSEQH---MWNLIELTNLNGTQFDPTDDVPAPlGVPDFAGEVFGVLQSQRNRGESNPAN 348  
 300 : TDSP-QARDHPLHVQVKNLDCTYDPTDDIPAVLGAIDFKGTVFGVASQRD-VSGPQEQQ 357  
 300 : TDSP-QARARNHPLHVQVKNLDCTYDPTDDIPAVLGAIDFKCTVFGVASQRD-VSGQQEQ 357  
 291 : QTRLADQPN-YTYQVHLENLDGSQVDPTDEVPAPlGTPDFQAQLFVGVISQR-----S 341  
 291 : TQQVQDEHRCGTHWNMTVTNLNGTPFDPTEDVPAPLGTDPDFSGQIYGVISQRNTNTVPEG 350  
 291 : NQKVSGENH---VWNMQVTNINGTPFDPTGDVPAPlGTPDFSGKLFVGVLQSQRD---HDNAC 345  
 290 : -TVADNGDNDQNLQLTYPNGASYDPTDEVPAPlGTPQDFSGMLYGVLTQ-----DNVNVS 344  
 291 : TTHLADDRH---LWN1IQVSNLNGLNGTPFDPTDDVPAPlGMPDFSGQIFGVVSQRDTG-TNPAN 347  
 301 :ADERAVGSF-DVW-VRLQEPDGGQPYDIFGKQPAPIGTPDFKAIVGFAAR-----P 349

Fig. 1-7

4 8 5 (G 2 / 1)  
 NG 1 (G 2 / 2)  
 MK 0 4 (G 2 / 2)  
 3 3 6 (G 2 / 3)  
 1 8 - 3 (G 2 / 3)  
 8 0 9  
 1 0 4 (G 2 / 4)  
 2 0 0 6 a (Aomori) (G 2 / 4)  
 2 0 0 6 b (Saga) (G 2 / 4)  
 2 0 0 7 a (G 2 / 4)  
 2 0 0 8 a (Apel door \_ 3 1 7 \_ NL \_ 2 0 0 7 )  
 2 0 0 8 a (Miyoshi 1 G 2 - 4 )  
 2 0 0 9 a (New)  
 7 5 4 (G 2 / 5)  
 4 4 5 (G 2 / 6)  
 7 k (G 2 / 6)  
 U 2 5 (G 2 / 8)  
 V 1 e t 0 2 6 (G 2 / 1 0)  
 7 6 (G 2 / 1 2)  
 4 7 (G 2 / 1 4)  
 Kamo 8 (G 2 / 1 5)  
 Alpha 2 3 (G 2 / 1 7 )

3 4 6 : ---- RAHDG I LATWSPKFTPPLGSVVLGTWEDRDFDINQPT--- RFTPVGLY---- D--- T 3 9 2  
 3 4 9 : E - PANRGHDAVVPPTYTAQ YTPKLGQVQI GTWQTDLQLVNQPV--- KFTPVG --- NDT 3 9 9  
 3 4 9 : E - PANRGHDAVVPPTYTSQYTPKLGQI QIGT WQTDLTLVNQPV--- KFTPVG --- NDT 3 9 9  
 3 5 7 : ---- TRAEAKVDDTTSGRFTPPLGSLEIT - ESDDFNQNKP T--- RFTPVG I---- GVDNE 4 0 5  
 3 5 7 : ---- TRAEAKVDDTTSGRFTPPLGSLEIT - ESDDFDTNQST--- KFTPVG I---- GVDNE 4 0 5  
 3 5 7 : ---- TRAEAKVDDTTAGRFTPPLGSLEIST - DSDDFDQNQPT--- KFTPVG I---- GVDNE 4 0 5  
 3 4 0 : EDGSTRGHKATVSTGSVWHFTPKLGSVQYTTDNNDFQTGQNT--- KFTPVGVIQDG N - NHQ 3 9 6  
 3 4 0 : RDGSTRGHKATVSTGSVWHFTPKLGR I QFSTDTSNDFETGQNT--- RFTPVGVQDGSTTHQ 3 9 7  
 3 4 0 : GDGSTRGHKATVVTGSAFTPKLGSVQFSTDTEFDETHQNT--- KFTPVGVIQDGSTTHR 3 9 7  
 3 4 0 : SDGSTRGHKATVLTGSADFAPKLGRVQFATD TDNDFESGQNT--- KFTPVGVIQDGSTTHR 3 9 7  
 3 4 0 : ADGSTRGHKATVVTGSAADFAPKLGRVQFATD TDNDFDANQNT--- KFTPVGVIQDGNTAHR 3 9 7  
 3 4 0 : GDGSTRGHKATVVTGSAADFTPKLGSVQFGTDTENDFETHQNT--- KFTPVGVIQDGSTTHR 3 9 7  
 3 4 0 : TDGSTRGHKATVVTGSADFS PKLGRVQFATD TDNDFDANQNT--- KFTPVGVIQDG GTAHR 3 9 7  
 3 4 9 : ---- RAHDAVVATYSDKYTPKLGVLQIGTWNNTD - VENQPT--- KFTPPIGLN --- EVANG 3 9 7  
 3 5 8 : GHYATRAHEAHIDTTDPKYAPKLGTILIKS - ESNDFITNQPI --- RFTPVG M --- G --- D 4 0 7  
 3 5 8 : GHYATRAHEAHIDTTDPKYAPKLGTILIKS - GSDDFNTNQPI --- RFTPVG M --- G --- D 4 0 7  
 3 4 2 : SDNATRAHEARVNTNDPTFAPQIAQVRFKS - PSNDFFDNEPI --- SVDSQ 3 9 4  
 3 5 1 : NL PANRAHEAVIATYSPKFTPPLGN1QFSTWETQDVSSCQPT--- KFTPVG LA --- SVDAN 4 0 5  
 3 4 6 : ---- RSHDAVIATNSAKFTPPLGA1QIGTWEEDDVHNQPT--- KFTPVG LF --- E --- N 3 9 2  
 3 4 5 : TGEAKNAKG YI STTSGKFTP KIGSIGLHS - I TEHVHPNQQS --- RFTPVG V --- AVDEN 3 9 7  
 3 4 8 : ---- RAHD AVALAT YSAKYTPKLGSVQI GTW DTE DLLER QP V --- KFTPVG LN --- E1GQD 3 9 7  
 3 5 0 : LTSGSYANEAYVNTTASDYAPATGNMRFTVRNGGTGH I SANKYWEFKSFGV --- EGERHTN 4 0 7

Fig. 1-8

4 8 5 (G2/1) PL FPGE QLLFFRSYIPL--KGGT--SNGAIDCLL 4 4 8  
 NG1 (G2/2) PV FPGE RLLFFRSYIPL--KGGY--GNPAIDCLL 4 5 5  
 MK0 4 (G2/2) PV FPGE RLLFFRSYIPL--KGGY--GNPAIDCLL 4 5 5  
 3 3 6 (G2/3) PV FPGE QLLFFRSQLPS--SNGILDCLV 4 6 1  
 1 8 - 3 (G2/3) PV FPGE QLLFFRSQLPS--SNGVLDCLV 4 6 1  
 8 0 9 4 0 6 : AEFQQQWSQLPDSQQFTHNMNLAPAVA P N FPGE QLLFFRSQLPS--SNGVLDCLV 4 6 1  
 1 0 4 (G2/4) 4 0 6 : AEFQQQWSQLPDSQQFTHNMNLAPAVA P N FPGE QLLFFRSQLPS--SNGVLDCLV 4 6 1  
 2 0 0 6 a (Aomori 1) (G2/4) 3 9 7 : NEPQQQWVLPPNYSGRDSSHNVHLAPAVA P T FPGE QLLFFRSTMPG--CSGY--PNMMLDCLL 4 5 2  
 2 0 0 6 b (Saga) (G2/4) 3 9 8 : NEPQQQWVLPPNYSGRDSSHNVHLAPAVA P S FPGE QLLFFRSTMPG--CSGY--PNMMLDCLL 4 5 3  
 2 0 0 7 a (G2/4) 3 9 8 : NEPQQQWVLPPNYSGRTGHNVHLAPAVA P T FPGE QLLFFRSTMPG--CSGY--PNMMLDCLL 4 5 3  
 2 0 0 8 a (Ape door\_3117\_NL\_2 0 0 7) 3 9 8 : NEPQQQWVLPPNYSGRNVMNVHLAPAVA P T FPGE QLLFFRSTMPG--CSGY--PNMMLDCLL 4 5 3  
 2 0 0 8 a (Miyoshi G2-4) 3 9 8 : NEPQQQWVLPPNYSGRNVMNVHLAPAVA P T FPGE QLLFFRSTMPG--CSGY--PNMMLDCLL 4 5 3  
 2 0 0 9 a (New) 3 9 8 : HRFEQWTLPPRSYSGALTNMNLAPAVA P L FPGE RLLFFRSYVPL--KGGF--GNPAIDCSV 4 5 3  
 7 5 4 (G2/5) 4 0 8 : NNWRQWELPDYSGRLTNMNLAPAVS P S FPGE R1LFFRSIVPS--AGGY--GSGYIDCLL 4 6 3  
 4 4 5 (G2/6) 4 0 8 : NNWRQWELPDYSGRLTNMNLAPAVS P S FPGE R1LFFRSIVPS--AGGY--GSGYIDCLL 4 6 3  
 7 k (G2/6) 3 9 5 : NSYNQWLLPRYGGHLTNNTHLAPS SV P M FPGE Q1LFFRSFMPG--ASGH--TDGAIDCLL 4 5 0  
 U2 5 (G2/8) 4 0 6 : SHFDQWTLPPSYSGALTNMNLAPAVA P V FPGE C1LFFRSF1PL--KGGY--GNPAIDCLM 4 6 1  
 V1 et 0 2 6 (G2/1 0) 3 9 3 : EGFNQWTLPPNYSGALTNMGLAPPVA P T FPGE Q1LFFRSYIPL--KGGV--ADPV1DCLL 4 4 8  
 7 6 (G2/1 2) 3 9 8 : TPPQQQWVLPPHYAGSLAINTNLAPAVA R L SLVS NCCSSGPVSHV--FKAYRGQDAF1DCLL 4 5 5  
 4 7 (G2/1 4) 3 9 8 : KHFDDQWVLPPNYSGALGLNMHLAPAVS P L FPGE RLLFFRSYIPL--KGGH--GDPF1DCLL 4 5 3  
 Kamo 8 (G2/1 5) 4 0 8 : IQYQEYELPDYSGQVASNHNLAPPVA P R MPGE SLLLFSQSSMPVWDDCHGESTPKKIHCCLL 4 6 7  
 Alpha 2 3 (G2/1 7)

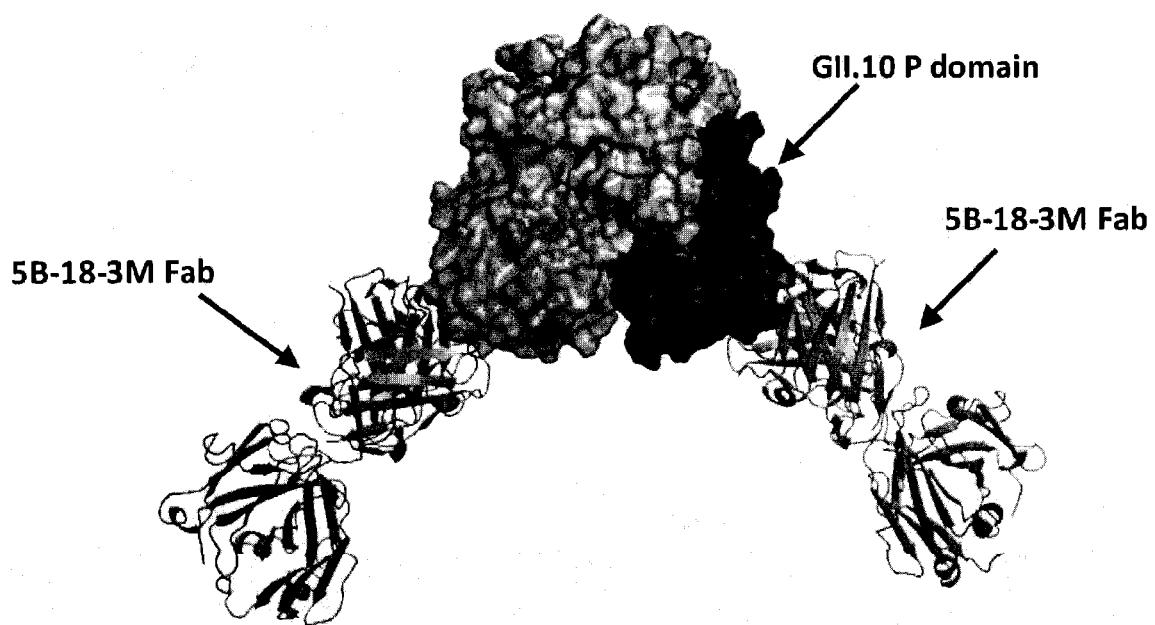
Fig. 1-9

485 (G2/1) 449 : PQEWVQHFYQEAPSSSTDVALIYTNPDGTGRVLFE AKLHRQGFITVANSGRPIVVPPNG 508  
 NG1 (G2/2) 456 : PQEWVQHFYQEAPSMSSEVALVRYINPDGTGRALFE AKLHRAGFVTVSSNTSAPVVVPANG 515  
 MK04 (G2/2) 456 : PQEWVQHFYQEAPSMSSEVALVRYINPDGTGRALFE AKLHRAGFMTMVSNTSAPVVVPANG 515  
 336 (G2/3) 462 : PQEWVQHFYQEAPQTQVALVRYNPDGTGRVLFE AKLHKMGMFTIAKNGDSPITVPPNG 521  
 18-3 (G2/3) 462 : PQEWVQHFYQEAPQTQVALVKYVNPDGTGRVLFE AKLHKLGFMITAANNGDSPITVPPNG 521  
 809 462 : PQEWVQHFYQEAPQTQVALVRYVNPDGTGKVLFE AKLHKLGFMITAANNGDSPITVPPNG 521  
 104 (G2/4) 453 : PQEWVQHFCQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGPHDLVIPPNG 512  
 2006a (Aomori) (G2/4) 454 : PQEWVQHFYQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGGHDLVIPPNG 513  
 2006b (Saga) (G2/4) 454 : PQEWVQHFYQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGGHDLVIPPNG 513  
 2007a (G2/4) 454 : PQEWVQHFYQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGGHDLVIPPNG 513  
 2008a (Apeldoorn\_317\_NL\_2007) 454 : PQEWVQHFYQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGGHDLVIPPNG 513  
 2008a (Miyoshi) (G2/4) 454 : PQEWVQHFYQEAAPAQSVALLRFVNPDGTGRVLFE CKLHKSGGYVTTVAHTGGHDLVIPPNG 513  
 2009a (New) 454 : PQEWVQHFYQEAPSLGDVALVRYVNPDGTGRVLFE AKLHKGGFLTVSSSTGPPVVVPANG 513  
 754 (G2/5) 464 : PQEWGQHFYQEAAAPSQSVALVRYVNPDGTGRNLFE AKLHREGFLTVANSGNNPIVVPPNG 523  
 445 (G2/6) 464 : PQEWVQHFYQEAAAPSQSVALVRYVNPDGTGRNLFE AKLHREGFLTVANCNNPIVVPPNG 523  
 7k (G2/6) 451 : PQEWVAHFYQEATAQTDVALIYTNPDGTGRVLFE GKLHKQGFITISNSGDPILVMPANG 510  
 U25 (G2/8) 462 : PQEWVQHLYQEAPSLSDVALVRYVNPDGTGRTLFE AKLHRNGFLTVARNSAGPVVAPTNG 521  
 Viet026 (G2/10) 449 : PQEWIQLYQEAPTSQSDVALIRFTNPDGTGRVLFE AKLHRSGYITVANTGSRPIVVVPANG 508  
 76 (G2/12) 456 : PQEWVNHFYQEAAAPSQADVALIYVNPDGTGRTLFE AKLHRSGFITVSHTAGYPLVVPNG 515  
 47 (G2/14) 454 : PQEWIQLHKEGFIITVSSTENRPVIVPPNG 513  
 Kamo8 (G2/15) 468 : PQEFIGHFFDKQAPSLSVALVRYVNQETNRVLFE CKLYRDGYITVAASSGL-LDFPLD 526  
 Alpha23 (G2/17)

Fig. 1-10

5 3 5	4 8 5 (G 2 / 1)	5 0 9 : YFRFDSW V N Q F YSL APM GTGN GRRV Q ---
	N NG 1 (G 2 / 2)	5 1 6 : YFRFDSW V N Q F YSL APM GAGN GRRV Q ---
	M MFK 0 4 (G 2 / 2)	5 1 6 : YFRFDSW V N Q F YSL APM GTGN GRRV Q ---
	3 3 6 (G 2 / 3)	5 2 2 : YFRFESW V N P F YTL APM GTGK GRRI Q ---
	1 8 - 3 (G 2 / 3)	5 2 2 : YFRFESW V N P F YTL APM GTGN GRRI Q ---
8 0 9		5 2 2 : YFRFESW V N P F YTL APM GTGN GRRI Q ---
1 0 4 (G 2 / 4)	5 1 3 : YFRFDSW V N Q F YTL APM GNGA GRRAL ---	
	2 0 0 6 a (A o m o r 1) (G 2 / 4)	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRAL ---
	2 0 0 6 b (S a g a) (G 2 / 4)	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRAL ---
	2 0 0 7 a (G 2 / 4)	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRAV ---
	2 0 0 8 a (A p e l d o o r n _ 3 1 7 _ NL _ 2 0 0 7 )	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRAL ---
	2 0 0 8 a (M i y o s h i G 2 - 4)	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRVL ---
	2 0 0 9 a (N e w)	5 1 4 : YFRFDSW V N Q F YTL APM GNGT GRRAL ---
	7 5 4 (G 2 / 5)	5 1 4 : YFRFDSW V N Q F YSL APM GTGN GRRV Q ---
	4 4 5 (G 2 / 6)	5 2 4 : YFRFEAW V N Q F YTL APM GSGQ GRRAX ---
	7 K (G 2 / 6)	5 2 4 : YFRFEAW V N Q F YTL APM GSGQ GRRAQ ---
	U 2 5 (G 2 / 8)	5 1 1 : YFRFEAW V N Q F YSL APM GTGS GRRRI Q ---
	V i e t o 2 6 (G 2 / 1 0)	5 2 2 : YFRFDSW V N Q F YTL APM GNGS GRRM Q ---
	7 6 (G 2 / 1 2)	5 0 9 : YFRFDTW V N Q F YSL APM GTGN GRRV Q ---
	4 7 (G 2 / 1 4)	5 1 6 : HFRFDSW V N Q F YSL APM GTGN GRRRI Q ---
	K a m o 8 (G 2 / 1 5)	5 1 4 : YFRFDSW V N Q F YSL APM GTGN GRRV Q ---
A l p h a 2 3 (G 2 / 1 7)	5 2 7 : FFRFDSW V S S F YIL SPV GSGQ GRRGVRFQ	

Fig. 2



## ANTI-HUMAN NOROVIRUS GII ANTIBODY

## CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a 35 U.S.C. §371 national stage patent application of International patent application PCT/JP2012/073511, filed on Sep. 13, 2012, published as WO/2013/039165 on Mar. 21, 2013, the text of which is incorporated by reference, and claims the benefit of the filing date of Japanese application no. 2011-199059, filed on Sep. 13, 2011, the text of which is also incorporated by reference.

## TECHNICAL FIELD

The present invention relates to an antibody to human norovirus GII and, more particularly, to an anti-human-norovirus GII antibody for detecting human norovirus GII in a specimen through an immunological assay.

## BACKGROUND ART

When a human is orally infected with a human norovirus, the virus proliferates in the duodenum and the upper portion of the small intestine, thereby triggering infectious gastroenteritis. In this case, epithelial cells of the small intestine near the duodenum fall, thereby causing symptoms including vomiting, diarrhea, and abdominal pain. The incubation period from infection with norovirus to the onset is about 12 hours to 72 hours (average 1 to 2 days), and excretion of the virus to the feces lasts about 1 to 3 weeks even after the symptoms have disappeared. In some cases, such virus excretion for longer than 7 weeks is reported. About 70% of reported cases of food poisoning are caused by norovirus infection.

A norovirus is a virus having no envelope and having a plus single-stranded RNA of about 7,500 bases as the genome thereof. The genome of the norovirus is reported to include three protein coding regions (ORFs): ORF1, coding for a non-structural protein relating to viral replication; ORF2, coding for a capsid structural protein (VP1); and ORF3, coding for a minor structural protein (VP2). Also, the norovirus is categorized into 5 groups: Genogroups I to V (GI to GV), on the basis of similarity of capsid gene sequence. Of these, noroviruses GI, GII, and GIV are main causal viruses for human infection. In particular, Genogroup I (GI) and Genogroup II (GII) have a genetic diversity, and a variety of viruses having different phylogenetic properties are detected in specimens from humans. Thus, Genogroup I and Genogroup II may be divided into 14 or more genotypes and 17 or more genotypes, respectively.

Detection of norovirus is carried out by detecting a capsid structural protein with an antibody through enzyme immunoassay (EIA) (see Non-Patent Document 1) or immunochromatography (Non-Patent Document 2). Thus, correct detection of a human norovirus antigen requires an antibody that responds to all the genotypes.

However, hitherto, an antibody that can recognize and respond to a common antigen region has not been readily obtained. Thus, a norovirus detection reagent is produced through combination of a plurality of antibodies to norovirus antigen peptides having a specific amino acid sequence or to fragments thereof (see, for example, Patent Document 1), and noroviruses of different genotypes are individually detected.

Therefore, there is demand for creating an antibody that can comprehensively detect a wide variety of noroviruses GII of different genotypes.

## CITATION LIST

## Patent Document

5 Patent Document 1: JP-A-2009-542715

## Non-Patent Documents

10 Non-Patent Document 1: "The Evaluation of Improved Norovirus Antigen-Detection EIA Kits," Japanese Journal of Medicine and Pharmaceutical Science (monthly) Vol. 61, No. 1, p. 93-98 (Jan. 25, 2009)

15 Non-Patent Document 2: "The evaluation of Norovirus antigen rapid diagnostic kit "Quicknavi-Noro"," Japanese Journal of Medicine and Pharmaceutical Science (monthly) Vol. 61, No. 5, p. 779-785 (May 25, 2009)

## SUMMARY OF THE INVENTION

## Problems to be Solved by the Invention

An object of the present invention is to provide an anti-human-norovirus GII antibody which responds to substantially all genotypes of the human noroviruses belonging to GII and which can comprehensively detect such human noroviruses GII.

## Means for Solving the Problems

30 In order to attain the aforementioned object, the present inventor has studied to obtain an antibody which simultaneously responds to human noroviruses belonging to Genogroup GII, and has found that an antibody which binds to a particular site of the P (protruding) region of capsid protein of human norovirus GII can bind to a wide range of human noroviruses GII, whereby substantially all the human noroviruses GII of genotypes (GII/1 to GII/17) can be specifically detected.

Accordingly, the present invention is directed to the following (1) to (4):

40 (1) an anti-human-norovirus GII antibody that binds to at least one of epitopes which are contained in amino acid regions represented by the following formulas (1) and (2):

P-X<sup>1</sup>-X<sup>2</sup>-P-G-E (1) (SEQ ID NO: 2)

X<sup>3</sup>-X<sup>4</sup>-X<sup>5</sup>-F-Y-X<sup>6</sup>-L-X<sup>7</sup>-P-X<sup>8</sup> (2) (SEQ ID NO: 3)

45 (wherein, X<sup>1</sup> represents L, V, N, T, S, M, or R; X<sup>2</sup> represents F, Y, or M; X<sup>3</sup> represents V or G; X<sup>4</sup> represents N or S; X<sup>5</sup> represents Q, P, or S; X<sup>6</sup> represents S, T, or I; X<sup>7</sup> represents A or S; and X<sup>8</sup> represents M or V), and of an epitope formed of amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or an epitope formed of an amino acid corresponding to amino acid 483, the regions and the amino acids being present in the P domain of a capsid structural protein of a human norovirus GII.

50 (2) the anti-human-norovirus GII antibody according to (1) above, wherein the amino acid region represented by formula (1) is a region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1, or a region corresponding thereto, and the amino acid region represented by formula (2) is a region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1, or a region corresponding thereto;

55 (3) a human norovirus GII detection reagent containing an antibody as recited in (1) or (2) above; and

60 (4) a method for detecting a human norovirus GII, the method comprising reacting a specimen suspected to contain

the human norovirus GII with an antibody as recited in (1) or (2) above, and detecting the virus through immunological assay.

#### Effects of the Invention

By use of the anti-human-norovirus antibody of the present invention, the human noroviruses belonging to the group GII can be comprehensively detected, whereby a wide variety of human noroviruses of different genotypes belonging to GII can be detected comprehensively and effectively. Furthermore, since the anti-human-norovirus GII antibody of the present invention can bind to an amino acid region of the P domain, which region is thought to have less genetic mutation, the virus detection reagent using the antibody does not require antibody reconstruction so as to fit an epidemic type, which is advantageous.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1-1 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-2 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-3 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-4 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-5 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-6 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-7 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-8 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-9 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having 21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 1-10 An alignment chart of amino acid sequences of capsid structural proteins of human norovirus strains having

21 genotypes of GII. FIG. 1-1 to FIG. 1-10 disclose full length SEQ ID NOS 1 and 21-41, respectively, in order of appearance.

FIG. 2 A bonding state between an anti-norovirus GII monoclonal antibody (5B-18-3M) and the norovirus, obtained through X-ray crystallographic structural analysis.

#### MODES FOR CARRYING OUT THE INVENTION

In the present specification, alphabetical letters in the formulas for the amino acid regions represent symbols of amino acids in a one-letter manner. Each sequence is given from the N-terminal to the C-terminal (from left to right).

The anti-human-norovirus GII antibody of the present invention binds to at least one of the epitopes which are contained in amino acid regions represented by the following formulas (1) and (2):

P-X<sup>1</sup>-X<sup>2</sup>-P-G-E (1) (SEQ ID NO: 2)

X<sup>3</sup>-X<sup>4</sup>-X<sup>5</sup>-F-Y-X<sup>6</sup>-L-X<sup>7</sup>-P-X<sup>8</sup> (2) (SEQ ID NO: 3)

(wherein, X<sup>1</sup> represents L, V, N, T, S, M, or R; X<sup>2</sup> represents F, Y, or M; X<sup>3</sup> represents V or G; X<sup>4</sup> represents N or S; X<sup>5</sup> represents Q, P, or S; X<sup>6</sup> represents S, T, or I; X<sup>7</sup> represents A or S; and X<sup>8</sup> represents M or V), and of an epitope formed of amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or formed of an amino acid corresponding to amino acid 483, the regions and the amino acids being present in the P domain of a capsid structural protein of a human norovirus GII.

As used herein, the term "human norovirus GII" refers to a human norovirus belonging to GII (Genogroup II).

The capsid structural protein (VP1) of the human norovirus is known to be formed of a shell domain (S domain) and a protruding domain (P domain). The S domain is thought to control assembly of VP1. According to a certain study, the following is reported. The P domain is divided into P1 and P2 subdomains, wherein the P1 subdomain interacts with the S domain, to thereby potentiate physical stability of capsid, whereas the P2 subdomain is present at the outermost shell of each virus particle. In the case of a mouse norovirus, the P2 subdomain serves as a target for a neutralizing antibody.

The amino acid regions of the present invention represented by formulas (1) and (2), and amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or an amino acid corresponding to amino acid 483 are present in the P domain of capsid structural protein of a human norovirus GII. Therefore, conceivably, the amino acid regions and the amino acids have high sequence conservation for each genotype and have less genetic mutation. Hitherto, there has been known no antibody that recognizes such amino acid regions or amino acids.

In formula (1), P represents proline, G represents glycine, and E represents glutamic acid.

X<sup>1</sup> represents L (leucine), V (valine), N (asparagine), T (threonine), S (serine), M (methionine), or R (arginine).

X<sup>2</sup> represents F (phenylalanine), Y (tyrosine), S (serine), or M (methionine), with F being preferred.

Examples of preferred amino acid regions represented by formula (1) include the following (1-1) to (1-9):

P-L-F-P-G-E (1-1) (SEQ ID NO: 4),

P-V-F-P-G-E (1-2) (SEQ ID NO: 5),

P-N-F-P-G-E (1-3) (SEQ ID NO: 6),

P-T-F-P-G-E (1-4) (SEQ ID NO: 7),

P-S-F-P-G-E	(1-5) (SEQ ID NO: 8),
P-T-Y-P-G-E	(1-6) (SEQ ID NO: 9),
P-M-F-P-G-E	(1-7) (SEQ ID NO: 10),
R-L-S-L-V-S	(1-8) (SEQ ID NO: 11), and
P-R-M-P-G-E	(1-9) (SEQ ID NO: 12).

In formula (2), F represents phenylalanine, Y represents tyrosine, L represents leucine, and P represents proline.

X<sup>3</sup> represents V (valine) or G (glycine), with V being preferred.

X<sup>4</sup> represents N (asparagine) or S (serine), with N being preferred.

X<sup>5</sup> represents Q (glutamine), P (proline), or S (serine), with Q being preferred.

X<sup>6</sup> represents S (serine), T (threonine), or I (isoleucine), with S or T being preferred.

X<sup>7</sup> represents A (alanine) or S (serine), with A being preferred.

X<sup>8</sup> represents M (methionine) or V (valine), with M being preferred.

Examples of preferred amino acid regions represented by formula (2) include the following (2-1) to (2-8):

V-N-Q-F-Y-S-L-A-P-M	(2-1) (SEQ ID NO: 13),
V-N-P-F-Y-T-L-A-P-M	(2-2) (SEQ ID NO: 14),
V-N-Q-F-Y-T-L-A-P-M	(2-3) (SEQ ID NO: 15),
V-N-Q-F-Y-T-L-A-P-V	(2-4) (SEQ ID NO: 16),
V-N-Q-F-Y-S-L-A-P-M	(2-5) (SEQ ID NO: 17),
G-N-Q-F-Y-T-L-A-P-M	(2-6) (SEQ ID NO: 18),
V-N-Q-F-Y-S-L-A-P-V	(2-7) (SEQ ID NO: 19), and
V-S-S-F-Y-I-L-S-P-V	(2-8) (SEQ ID NO: 20).

The amino acid region represented by the above formula (1) or (2) is present in the P domain of capsid structural protein of human norovirus GII. In the case of 485 strain of genotype GII/1, the amino acid region represented by formula (1) corresponds to an amino acid region from amino acid residue 419 to amino acid residue 424 of the amino acid sequence represented by SEQ ID NO: 1, and the amino acid region represented by formula (2) corresponds to an amino acid region from amino acid residue 516 to amino acid residue 525 of the amino acid sequence represented by SEQ ID NO: 1.

In the present invention, the amino acid region corresponding to the region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1, the amino acid region corresponding to the region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1, and the amino acid corresponding to amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1 mean, for example, regions or amino acid corresponding to the region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1, the region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1, and amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, which are given through alignment with each genotype based on the amino acid sequence of the VP 1 of genotype GII/1 485 strain by means of genetic information processing software GENETYX (see FIG. 1). Through align-

ment of the amino acid sequence of VP1 through such a method, a specific region of the amino acid sequence in the P domain of each human norovirus GII can be determined, even when a deletion is present in the amino acid sequence. A corresponding homologous region is thought to be present in the same region in the 3-dimensional structure, indicating the possible presence of the same epitope of human norovirus GII.

In the case of NG1 strain shown in FIG. 1, the region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1 corresponds to a region from amino acid 426 to amino acid 431; the region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1 corresponds to a region from amino acid 523 to amino acid 532; and amino acid 483 corresponds to amino acid 490.

The anti-human-norovirus GII antibody of the present invention binds to an epitope contained in the aforementioned amino acid region or to an epitope formed of the amino acid.

As used herein, the term "epitope" refers to an antigenic determinant and, more specifically, to a structural site specifically binding to an antibody. The epitope of the present invention may be a consecutive amino acids of a part of the amino acid region or amino acids present discretely in the region.

Also, the term "binding" refers to an interaction between a ligand and a substrate, which may be differentiated from a background or a non-specific or specific interaction.

The anti-human-norovirus GII antibody of the present invention at least binds to an epitope contained in the amino acid region represented by the aforementioned formula (1) or (2), or to an epitope formed of amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or to an epitope formed of an amino acid corresponding to amino acid 483. Preferably, the antibody of the present invention can bind to all of the epitopes.

The epitope contained in the amino acid region represented by formula (1) is preferably "X<sup>1</sup>," and the epitope contained in the amino acid region represented by formula (2) is preferably "X<sup>4</sup>" and/or "Y-X<sup>6</sup>-L."

Thus, in the case of GII/1 genotype 485 strain, the epitope is preferably one or more selected from among L of amino acid 420 of the amino acid sequence represented by SEQ ID NO: 1 in the amino acid region represented by formula (1-1); N of amino acid 517, and Y-S-L of the region of amino acids 520 to 522, in the amino acid region represented by formula (2-1); and E of amino acid 483.

In the case of GII/1 genotype NG1 strain, the epitope is preferably one or more selected from among V of amino acid 427 of the amino acid sequence represented by SEQ ID NO: 1 in the amino acid region represented by formula (1-2); N of amino acid 524, and Y-S-L of the region of amino acids 527 to 529, in the amino acid region represented by formula (2-2); and E of amino acid 490.

As described in Table 1 hereinbelow, the anti-human-norovirus GII antibody can bind to substantially all of the following noroviruses belonging to the GII genogroup (GII/1 to GII/17): 485 strain, (GII/1), NG1 strain (GII/2), 809 strain (GII/3), 18-3 strain (GII/3), 336 strain (GII/3), 104 strain (GII/4), 754 strain (GII/5), 7k strain (GII/6), 445 strain (GII/6), 10-25 strain (GII/7), U25 strain (GII/8), 876 strain (GII/12), NG15 strain (GII/13), 47 strain (GII/14), Kamo strain (GII/15), and Alph strain (GII/17). However, the anti-human-norovirus GII antibody does not bind to a norovirus belonging to the GI genogroup.

No particular limitation is imposed on the species of the animal from which the anti-human-norovirus GII antibody of

the present invention is obtained. Among such animals, rat is preferred from the viewpoint of ease in production of the antibody.

The anti-human-norovirus GII antibody of the present invention may be of any required form such as IgG, IgA, IgY, IgD, IgM, IgE, or a part of one or more of these; e.g., a heavy chain, a light chain, Fc, or F(ab).

The anti-human-norovirus GII antibody employed in the present invention may be obtained, through known means, as a polyclonal antibody or a monoclonal antibody. Monoclonal antibodies derived from a mammal include those produced by a hybridoma, and those produced by a host genetically transformed with an expression vector containing the corresponding antibody gene.

Generally, such a hybridoma producing an anti-human-norovirus antibody may be produced through a known technique in the following manner. Specifically, recombinant GII norovirus-like particles (VLPs) are used as a sensitizing antigen, and are immunized though a routine immunization method. The thus-produced immunocytes are fused with known parent cells through a conventional cell fusion method. Then, through a conventional screening method, cells producing a monoclonal antibody are selected.

The recombinant norovirus GII VLP may be produced through the following procedure. Firstly, a gene sequence of capsid of a human norovirus GII is inserted into a transfer vector. SF9 cells are transfected simultaneously with baculovirus DNA and the aforementioned plasmid, whereby a recombinant virus is produced through homologous recombination. The recombinant virus is then proliferated, to thereby yield a seed virus. Subsequently, a protein is expressed in Tn5 cells, and a recombinant norovirus GII VLP is purified from the cells or a relevant culture supernatant through a known method.

No particular limitation is imposed on the mammal to be immunized with a sensitizing antigen, but the mammal is preferably selected in consideration of compatibility with parent cells to be used in cell fusion. Generally, rodents such as mouse, rat, and hamster are employed.

Immunization of an animal with a sensitizing antigen is carried out through a known method. In one procedure, a sensitizing antigen is intraperitoneally or subcutaneously injected to a mammal. More specifically, the sensitizing antigen is diluted and suspended with an appropriate amount of PBS (phosphate-buffered saline) or physiological saline. If needed, the suspension is mixed with an appropriate amount of a conventional adjuvant such as Freund's complete adjuvant. The thus-prepared suspension is emulsified, and the emulsion is administered subcutaneously, intradermally, or intraperitoneally to an animal for temporary stimulation. The operations are repeated in accordance with needs. The amount of antigen to be administered is appropriately determined depending on the administration route and the species of the animal. Generally, the unit dose is preferably about 10 µg to about 1 mg. After immunization and confirmation of rise in serum level of an antibody of interest, blood is collected from the mammal. Through purification of serum components, a polyclonal antibody can be produced. In purification of serum components, an affinity column to which a sensitizing antigen has been fixed or the like may be employed.

For producing a monoclonal antibody, immunocytes are removed from the antibody-level-elevated mammal and subjected to cell fusion. Among immunocytes, splenic cells are particularly preferred in cell fusion.

Myeloma cells of a mammal, which are counter parent cells to be fused with the aforementioned immunocytes,

include known cell strains such as P3x63, NS-1, MPC-11, and SP2/0. Myeloma cells of these strains are appropriately used.

The cell fusion between the immunocytes and myeloma cells may be carried out in accordance with a known method, such as a method of Kohler et al. (Kohler et al., *Nature*, vol., 256, p. 495-497 (1975)). Specifically, immunocytes and myeloma cells are mixed together in a nutrient culture medium such as RPMI1640 culture medium or MEM culture medium, in the presence of a cell fusion promoter such as polyethylene glycol (PEG: average molecular weight: 1,000 to 6,000, concentration: 30 to 60%) or Sendai virus (HVJ) with an optional promoter aid such as dimethyl sulfoxide, to thereby form hybridomas.

The hybridomas formed through cell fusion are cultured in a selective medium such as a medium containing hypoxanthine, thymidine, and aminopterin (HAT medium) for 1 to 7 days, and separated from unfused cells. Hybridomas producing an antibody of interest are further selected. The thus-selected hybridoma(s) is(are) monoclonized through a known limiting dilution analysis method, to thereby establish a monoclonal-antibody-producing hybridoma.

The activity of the antibody produced by the hybridoma may be detected through a known method, such as ELISA, an agglutination reaction method, or radioimmunoassay.

A target monoclonal antibody may be recovered from the thus-produced hybridoma through, for example, a method including culturing the hybridoma through a routine method and collecting the culture supernatant or a method including administering the hybridoma to a mammal compatible therewith, proliferating the hybridoma, and collecting the ascites of the mammal.

The target antibody may be purified through known purification means such as salting out, gel filtration, ion-exchange chromatography, or affinity chromatography.

When the anti-human-norovirus antibody of the present invention is applied to an immunological assay method, human norovirus GII present in a specimen can be specifically detected and measured.

No particular limitation is imposed on the immunological assay method, but a sandwich method employing an anti-norovirus GII antibody and a labeled anti-norovirus GII antibody is preferred. A sandwich method employing an immobilized anti-norovirus GII antibody and a labeled anti-norovirus GII antibody is more preferably employed.

Examples of preferred immobilized anti-norovirus GII antibodies include those immobilized on an insoluble support such as a polystyrene plate, latex particles, magnetic particles, a glass fiber membrane, a nylon membrane, a nitrocellulose membrane, or an acetylcellulose membrane.

Examples of the label of the labeled anti-human-norovirus GII antibody which may be used in the invention include known labels, such as radioisotopes (e.g.,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , and  $^3\text{H}$ ), enzymes (e.g., peroxidase, alkaline phosphatase, and luciferase), proteins (e.g., avidin), low-molecular-weight compounds (e.g., biotin), fluorescent substances (e.g., FITC), chemiluminescent substances (e.g., acridinium), latex particles (e.g., colored latex particles and fluorescent latex particles), metal (e.g., noble metals (e.g., gold, silver, and platinum)) colloid particles, and carbon atoms.

Norovirus GII present in a specimen is detected on the basis of reaction between the norovirus present in the specimen and an immobilized anti-norovirus GII antibody. In the case of sandwich assay, a specimen-containing liquid is reacted with an immobilized anti-norovirus GII antibody, and then with the aforementioned labeled antibody. Alternatively, a specimen-containing liquid may be reacted simultaneously

with an immobilized anti-norovirus GII antibody and the labeled antibody. After completion of reaction, the level of the label present in a complex formed of the norovirus present in the specimen, the immobilized anti-norovirus GII antibody, and the labeled antibody is measured, whereby the norovirus GII level of the specimen can be determined. The amount of the label may be measured through means depending on the type of the label. In the case where an enzyme or avidin is used as a label, a substrate is added after reaction, and the enzyme activity is measured. In the case where a fluorescent substance (including fluorescent latex particles) or a chemiluminescent substance is used as a label, signals are measured under such conditions that no quenching occurs. In the cases of colored latex particles, metal colloid particles, carbon particles, etc., signals are measured visually or by reflected light or the like.

In the present invention, norovirus GII is more preferably detected through ELISA or immunochromatography.

The detection reagent (kit) containing the anti-human-norovirus GII antibody of the present invention preferably contains an immobilized anti-human-norovirus GII antibody of the present invention, a diluent for a specimen, a labeled anti-norovirus GII antibody, a reaction substrate, and other components.

## EXAMPLES

### Example 1

#### Preparation of Anti-Norovirus GII Monoclonal Antibody

The antibody employed in the method of the present invention was produced through the following procedure.

Mice were immunized several times with GII norovirus-like particles (VLPs) (50 µg) by administering a mixture of VLPs and an adjuvant to the abdominal cavity of each mouse. A rise in serum titer was confirmed. The mice were boosted (via intravenous administration), and 3 days after the booster, the spleen was removed from each mouse, to thereby obtain splenic cells. The cells were fused with mouse myeloma cells (10:1 by no. of cells) in the presence of polyethylene glycol 3500, to thereby produce hybridoma cells. The cells were cultured for one week at 37°C. under CO<sub>2</sub>, and the presence of anti-norovirus antibody in a culture supernatant was checked. Cells in a positive well where production of the antibody was observed were diluted through the limiting dilution method, and the cells were cultured for 2 weeks. Then, the presence of anti-norovirus antibody in a culture supernatant was checked again. Thereafter, cells in a positive well where production of the antibody was observed were diluted again through the limiting dilution method, and the same culturing was performed. In this stage, the cells which were able to produce an anti-norovirus antibody were cultured in a flask. A part of the culture was suspended in 10% dimethyl sulfoxide (DMSO)-containing fetal calf serum (FCS) (5×10<sup>6</sup> cells/mL), and the suspension was stored in liquid nitrogen.

The reactivity of the produced antibodies in a culture supernatant of each well to norovirus was investigated. The norovirus-like particles (VLPs) were dissolved in 140 mM NaCl, 2.7 mM KCl, 10 mM Na<sub>2</sub>HPO<sub>4</sub>, and 1.8 mM KH<sub>2</sub>PO<sub>4</sub>, pH: 7.3 (hereinafter abbreviated as PBS, pH7.3). The norovirus-like particle (VLP)/PBS, pH7.3 solution was added to the wells of a plastic microtiter plate (Nunc-Immunot™ Module F8 Maxisorp™ Surface plate, product of Nalge Nunc International) at 100 µL/well. The norovirus-like particles (VLPs)

were immobilized on the microtiter plate under the conditions of 0.05 µg/well, at 4°C., for 12 hours. Twelve hours after immobilization, the norovirus-like particle (VLP)/PBS, pH7.3 solution added to the wells was removed through decantation. To the wells of the microtiter plate, 145 mM NaCl, 3.6 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.4 mM KH<sub>2</sub>PO<sub>4</sub>, and 0.05% (v/v.) Tween20 (hereinafter abbreviated as PBS-T) were added at 200 µL/well, and PBS-T was decanted out, to thereby wash excess norovirus-like particles (VLPs) adsorbed in the well.

The washing step was performed twice in total.

Subsequently, 145 mM NaCl, 7.2 mM Na<sub>2</sub>HPO<sub>4</sub>, 2.8 mM KH<sub>2</sub>PO<sub>4</sub>, 1% (wt./v.) BSA, and 5% (wt./v.) lactose (hereinafter the solution is referred to as antigen-immobilized plate blocking solution) were added to the wells of the plate at 200 µL/well, to thereby perform blocking in the wells of norovirus-like particle (VLP)-immobilized microtiter plate at 4°C. for 12 hours. Twelve hours after blocking, the microtiter plate was maintained at 4°C. The reactivity of the antibodies in a culture supernatant was checked by use of the norovirus-like particle (VLP)-immobilized microtiter plate after completion of blocking. To the wells of the norovirus-like particle (VLP)-immobilized microtiter plate, a supernatant of a hybridoma culture was added at 100 µL/well, and the plate was heated at 37°C. for one hour. Subsequently, the culture supernatant added to the wells was removed through decantation. Then, PBS-T was added to the wells of the microtiter plate at 200 µL/well, and PBS-T was decanted out for washing. The washing step was performed thrice in total.

Subsequently, peroxidase-conjugated goat anti-mouse immunoglobulins (product of DAKO) were added to the wells at 100 µL/well (dilution factor of 2,000: 0.55 µg/mL), and the plate was heated at 37°C. for one hour. The enzyme-labeled antibodies were diluted with 145 mM NaCl, 3.6 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.4 mM KH<sub>2</sub>PO<sub>4</sub>, 0.05% (v/v.) Tween 20, and 0.5% (wt./v.) BSA (hereinafter may be referred to as enzyme-labeled antibody dilution diluent). Then, the enzyme-labeled antibodies added to the wells were removed through decantation. PBS-T was added to the wells of the microtiter plate at 200 µL/well, and PBS-T was decanted out for washing. The washing step was performed thrice in total. Subsequently, 3,3',5,5'-tetramethylbenzidine (hereinafter abbreviated as TMB) solution (TMB One-Step Substrate System, product of DAKO) serving as a peroxidase enzymatic reaction substrate solution was added to the wells at 100 µL/well, and the plate was maintained at 25°C. for 30 minutes. Immediately after, 313 mM H<sub>2</sub>SO<sub>4</sub> solution (hereinafter may be referred to as reaction-terminating solution) was added to the substrate reaction liquid in the wells at 100 µL/well, to thereby terminate enzymatic reaction in the wells.

The absorbance of each well was measured at 450 nm and 630 nm, and the difference between the measurements at 450 nm and 630 nm was employed as an index for assessing reactivity (Josephy P. D., Mason R. P., et al. (1982), J. Biol. Chem. 257, 3669-3675). Meanwhile, many have reported about colorimetric analysis using TMB, since the first such report by Bos E. S. et al. in 1981 (Bos E. S. et al. (1981), J. Immunoassay. 2, 187-204). Therefore, the technique has been established on a reliable basis.

As a result, monoclonal hybridoma cells exhibiting high reactivity of anti-norovirus antibody to the immobilized norovirus-like particles (VLPs) were selected. The class and subclass of the immunoglobulin in the culture supernatant (100 µL) were determined by means of Immunoglobulin Typing Kit, Mouse (product of Wako Pure Chemical Industries, Ltd.) in terms of each clone. On the basis of the results, only

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the IgG class of the thus-obtained monoclonal cell library was subjected to the ascites method, according to the following procedure.

Specifically, these cells were cultured in a 25-mL flask and then in a 75-mL flask. The cultured cells were intraperitoneally injected to pristane-treated mice, and ascites was collected therefrom.

In selection of monoclonal hybridoma cells, monoclonal hybridoma cells exhibiting high reactivity of anti-norovirus antibody to the P-domain of the immobilized norovirus-like particles (VLPs) are selected instead of monoclonal hybridoma cells exhibiting high reactivity of anti-norovirus antibody to the immobilized norovirus-like particles (VLPs), whereby a hybridoma that can produce a monoclonal antibody that can bind to an amino acid region in the P domain can be selected at high reproducibility.

In selection of monoclonal hybridoma cells, the bonding state between the monoclonal antibody and norovirus is confirmed through the same method as described in Example 3 hereinbelow, whereby a hybridoma that can produce a monoclonal antibody that can bind to an amino acid region in the P domain can be selected at high reproducibility.

In the method employed in Example 1, the P-domain protein of norovirus-like particles (VLPs) is immunized instead of GII norovirus-like particles (VLPs), whereby a hybridoma that can produce a monoclonal antibody that can bind to an amino acid region in the P domain can be obtained at high reproducibility. A method for obtaining the P-domain protein is described in Example 3.

According to the present invention, the amino acid regions represented by formulas (1) and (2) and amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1 or an amino acid sequence corresponding thereto are selected, and a polypeptide formed of the amino acid sequences is produced therefrom. Through immunization with the polypeptide, a hybridoma that can produce a monoclonal antibody that can bind to an amino acid region in the P domain can be obtained at high reproducibility.

The polypeptide may be used as an antigen of human norovirus GII.

<Purification of Anti-Norovirus GII Monoclonal (IgG) Antibody>

The thus-obtained ascites (10 mL) was mixed with a turbid serum treatment agent (FRIGEN (registered trademark) II, product of Kyowa Pure Chemical Co., Ltd.) at a volume ratio of 1.5:1, and the mixture was stirred with shaking for 1 to 2 minutes, to thereby defat the ascites. The thus-treated ascites was centrifuged by means of a centrifuge at 3,000 rpm (1,930×g) for 10 minutes, to thereby recover a clear ascites centrifugation supernatant (10 mL). The ascites centrifugation supernatant (10 mL) was fractionated with ammonium sulfate (final concentration: 50%; ammonium sulfate saturation) for one hour in an ice bath, and a precipitated immunoglobulin fraction was suspended and dissolved in PBS. The ammonium sulfate fractionation was performed twice in total, to thereby recover a crude immunoglobulin fraction from the ascites. The thus-obtained crude immunoglobulin fraction (10 mL) was mixed with an equiamount of 20 mM sodium phosphate, pH: 7.0 (hereinafter referred to as 20 mM NaPB, pH7.0), and the mixture was purified through an affinity column; Protein G column (HiTrap Protein G HP, 5 mL: product of Amersham BioSciences). Specifically a sample was caused to be adsorbed onto a Protein G column, and then, 20 mM NaPB, pH7.0 (50 mL) was caused to pass through the Protein G column, to thereby remove miscellaneous matters other than IgG contained in the sample. Thereafter, IgG adsorbed on Protein G column was eluted with 0.1 M glycine-

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HCl, pH2.7. A fraction immediately after start of elution through the column was neutralized with 1 M tris(hydroxymethyl)aminomethane-HCl, pH9.0 (hereinafter, tris(hydroxymethyl)aminomethane is abbreviated as Tris), and the neutralized product was recovered. After neutralization, the affinity purified product was dialyzed against a 500-fold volume of PBS at 4° C. for 6 hours. The dialysis was performed twice in total. In dialysis, a cellulose tube for dialysis (product of Viskase Companies) was employed as a dialysis membrane. The thus-recovered IgG fraction was employed as an anti-norovirus GII monoclonal antibody (5B-18-3M) purified product, and the product was stored at 4° C. and used in the subsequent procedure. Notably, all the purification steps were performed by means of the aforementioned Protein G column connected to BioLogic LP system (product of Bio Rad Laboratories) at a flow rate of 1 mL/min.

### Example 2

#### Reactivity of Anti-Norovirus GII Monoclonal Antibody

By use of the anti-norovirus GII monoclonal antibody (5B-18-3M) produced in Example 1, norovirus GII detection reagents employing an immunochromatographic method were produced through the following procedure.

Firstly, a solution containing the anti-norovirus GII monoclonal antibody (5B-18-3M) in an amount of 0.36 to 1.45 mg/mL was applied onto a nitrocellulose membrane sheet in a line pattern so as to attain a coating amount of 0.25 to 1.00 µL/5 mm, to thereby provide test lines. A control line was provided through applying an anti-mouse globulin antibody in the same manner.

A solution containing latex to which the anti-norovirus GII monoclonal antibody (5B-18-3M) was bound in an amount of 0.04 to 0.15 w/v % was employed as an antibody-bound latex solution (5B-18-3M). A conjugate pad was impregnated with the latex solution and then dried.

A sample pad, the membrane, the conjugate pad, and an absorption pad were stacked in this order on a plastic backing sheet, such that adjacent members partially overlapped, and the stacked body was coated with a plastic laminate. The product was cut to a width of 5 mm, to thereby provide test strips.

The reactivity of the above-prepared reagent to a norovirus of each genotype was checked through the following procedure.

A recombinant antigen of each genotype of norovirus was suspended in a diluent, and the thus-obtained floating antigen (75 µL) was added dropwise to a sample pad of the above-produced test strip. The test strip was allowed to stand at 15 to 30° C. for 15 minutes, and then the presence of a line was checked. Table 1 shows the results. Note that 124 strain refers to Hu/NV/GI/Aichi124-89/89/JP (GeneBank accession number: AB031013) strain; 258 strain refers to Hu/NV/GI/Funabashi258/96/JP (GeneBank accession number: AB078335) strain; 645 strain refers to Hu/NV/GI/Kashiwa645/99/JP (GeneBank accession number: BD011871) strain; CV strain refers to Hu/NV/GI/Chiba407/87/JP (GeneBank accession number: AB042808) strain; W18 strain refers to Hu/NV/GI/WUG1/00/JP (GeneBank accession number: AB081723) strain; #8 strain refers to Hu/NV/GI/8/99/JP (GeneBank accession number: AB058547) strain; 485 strain refers to Hu/NV/GII/Noda485/00/JP (GeneBank accession number: unregistered) strain; NG1 strain refers to Hu/NV/GII/NG1/

02/JP (GeneBank accession number: AB195225) strain; 809 strain refers to Hu/NV/GII/Sanbu809/98/JP (GeneBank accession number: BD011876); 18-3 strain refers to Hu/NV/GII/Matsudo18/00/JP (GeneBank accession number: unregistered) strain; 336 strain refers to Hu/NV/GII/Kashiwa336/00/JP (GeneBank accession number: unregistered) strain; 104 strain refers to Hu/NV/GII/Narita104/97/JP (GeneBank accession number: unregistered) strain; 754 strain refers to Hu/NV/GII/Ichikawa754/98/JP (GeneBank accession number: BD011877) strain; 7k strain refers to Hu/NV/GII/Ueno7k/94/JP (GeneBank accession number: AB078337) strain; 445 strain refers to Hu/NV/GII/Sanbu445/00/JP (GeneBank accession number: unregistered) strain; 10-25 strain refers to Hu/NV/GII/Osaka10-25/99/JP (GeneBank accession number: BD011881) strain; U25 strain refers to Hu/NV/GII/SaitamaU25/\*\*/JP (GeneBank accession number: AB039780) strain; 1876 strain refers to Hu/NV/GII/Chitta/Aichi76-96/96/JP (GeneBank accession number: AB032758) strain; NG15 strain refers to Hu/NV/GII/NG15/03/JP (GeneBank accession number: unregistered) strain; 47 strain refers to Hu/NV/GII/Kashiwa47/97/JP (GeneBank accession number: AB078334) strain; Kamo strain refers to Hu/NV/GII/Kamo8/03/JP (GeneBank accession number: unregistered) strain; and Alph strain refers to Hu/NV/GII/Alph23/\*\*/JP (GeneBank accession number: unregistered) strain.

TABLE 1

Genogroup	Genotype	Virus strain	Reactivity
Genogroup I	GI/1	124	-
	GI/2	258	-
	GI/3	645	-
	GI/4	CV	-
	GI/6	W18	-
	GI/11	#8	-
Genogroup II	GII/1	485	+
	GII/2	NG1	+
	GII/3	809	+
	GII/3	18-3	+
	GII/3	336	+
	GII/4	104	+
	GII/5	754	+
	GII/6	7k	+
	GII/6	445	+
	GII/7	10-25	+
	GII/8	U25	+
	GII/12	1876	+
	GII/13	NG15	+
	GII/14	47	+
	GII/15	Kamo	+
	GII/17	Alph	+

As is clear from Table 1, the anti-norovirus GII monoclonal antibody (5B-18-3M) was able to bind to virtually all the noroviruses belonging to the GII genegroup divided into GII/1 to GII/17, including 485 strain (GII/1), NG1 strain (GII/2), 809 strain (GII/3), 18-3 strain (GII/3), 336 strain (GII/3), 104 strain (GII/4), 754 strain (GII/5), 7k strain (GII/6), 445 strain (GII/6), 10-25 strain (GII/7), U25 strain (GII/8), 1876 strain (GII/12), NG15 strain (GII/13), 47 strain (GII/14), Kamo strain (GII/15), and Alph strain (GII/17), and did not bind to noroviruses belonging to the GI genegroup.

## X-Ray Crystallographic Structural Analysis

In order to elucidate the bonding state between the anti-norovirus GII monoclonal antibody (5B-18-3M) and norovirus, the following X-ray crystallographic structural analysis was carried out.

## (1) Preparation of Samples

<Protein Expression of Norovirus P Domain, and Purification and Crystallization of Protein>

P domain (amino acid residues 224 to 538) (amino acid length: 314), which is similar to the full length of the P domain of norovirus Vietnam 026 GII.10, was designed for protein expression in *E. coli*. The designed P domain was inserted into a pMal-c2x vector obtained by cutting with restriction enzymes BamHI and NotI (product of New England Biolabs), to thereby produce a clone for protein expression. The clone was transformed to *E. coli* BL21 cells (product of Invitrogen), and protein expression was induced with IPTG (1 mM) at 22°C. for 18 hours. The thus-obtained His-tagged fusion P domain protein was purified with a Ni column (product of Qiagen) and treated overnight with HRV-3C protease (product of Novagen) at 4°C. Thereafter, the thus-treated liquid was caused to pass through the Ni column, to thereby purify the P domain.

The P domain was further purified through molecular sieve chromatography by use of Superdex 200 column (GE) and concentrated to 2 to 10 mg/mL. Before crystallization, the purified P domain was stored in GFB (0.35 M NaCl, 2.5 mM Tris, pH 7.0, 0.02% NaN<sub>3</sub>).

<Preparation of Fab Fragments of Anti-Norovirus GII Monoclonal Antibody (5B-18-3M)>

Fab fragments were prepared by use of the purified 5B-18-3M IgG (about 60 mg). Specifically, 5B-18-3M IgG was reduced with 100 mM dTT at 37°C. for one hour. The thus-reduced 5B-18-3M IgG was dialyzed in a dialysis cassette at 4°C. for one hour. Then, the buffer was changed to GFB containing 20 mM HEPES (pH: 7.7), and alkylation was performed with GFB containing 2 mM iodoacetamide at 4°C. for 48 hours. Subsequently, the cassette was transferred to new GFB containing no iodoacetamide, and the buffer was substituted at 4°C. for one hour. 5B-18-3M IgG was concentrated to 5 mg/mL, and digested with papain by means of a kit (pierce, Rockford, USA). The digested 5B-18-3M IgG was purified with Protein A column in terms of Fab. The Fab was further purified through molecular sieve chromatography by use of Superdex 200 column (GE) and concentrated to 5 mg/mL. The Fab was stored in GFB.

The thus-purified P domain of norovirus GII.10 and 5B-18-3M Fab were mixed together at 1:1, and the mixture was allowed to react at 25°C. for one hour. Finally, the reaction product was purified through molecular sieve chromatography.

<Co-Crystallization of a Complex of Norovirus P Domain and Fab of Anti-Norovirus GII Monoclonal Antibody (5B-18-3M)>

The aforementioned complex of the P domain of norovirus and Fab of the anti-norovirus GII monoclonal antibody (5B-18-3M) was crystallized under conditions slightly different from those employed in the hanging-drop vapor diffusion method using a reagent of Hampton Research Corp.

For the purpose of the research, a GII.10 P domain-Fab complex was mixed with GFB containing PEG 400 (40% v/v), PEG 3350 (5% w/v), and 0.1 M acetic acid (pH: 5.5) at a ratio of 1:1, to thereby grow crystals of a P-domain-Fab

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complex. Before data collection, the crystals were transferred to an anti-freezing agent; i.e., a mixture of 30% ethylene glycol containing GFB.

## (2) Structural Analysis

X-ray diffraction data of the crystalline complex of the anti-norovirus GII monoclonal antibody (5B-18-3M) and the P domain of norovirus GII.10 capsid protein were created by use of beam lines of Argonne National Laboratory (Argonne, Ill.): Southeast Regional Collaborative Access Team (SER-CAT) 22-ID and 22-BM. The diffraction data were processed by protein-low molecule data processing software HKL2000 with a program package XDS. In structural analysis, PDB (Protein Data Bank) code 1WEJ was used as a search model for Fab of the anti-norovirus GII monoclonal antibody, and PDB code 20BR was used as a search model for the P domain of norovirus capsid. The stearic structure was constructed by use of molecular substitution-based structural analysis software PHASER, from the diffraction data and the amino acid sequences of the anti-norovirus GII monoclonal antibody (5B-18-3M) and the P domain of norovirus GII.10 capsid protein.

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Thereafter, the stearic structure was refined with a manual model provided in model building software COOT and modified with a refining program REFMAC, TLS refinement, and automatic structure determination software PHENIX. By means of CCP4, superposition and root mean square deviation (RMSD) were calculated. Thus, the stearic structure was drawn by molecular graphic tool PyMOL.

## (3) Results

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Through the above procedure, the structure shown in FIG. 2 was obtained. Based on the thus-obtained structure, amino acid sequences of the P domain of norovirus GII.10 capsid protein in the site where the anti-norovirus GII monoclonal antibody (5B-18-3M) was bound to the P domain of GII.10 capsid protein were identified. As a result, three regions were found. Subsequently, homology in amino acid sequence was compared among respective noroviruses of different genotypes. As shown in FIG. 1, these three regions were highly conserved among the different genotypes.

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SEQUENCE LISTING

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&lt;160&gt; NUMBER OF SEQ ID NOS: 41

&lt;210&gt; SEQ ID NO 1

&lt;211&gt; LENGTH: 535

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: 485 strain (G2/1)

&lt;400&gt; SEQUENCE: 1

Met	Lys	Met	Ala	Ser	Asn	Asp	Ala	Ala	Pro	Ser	Asn	Asp	Gly	Ala	Ala
1			5				10							15	

Gly	Leu	Val	Pro	Glu	Val	Asn	Asn	Glu	Met	Met	Ala	Leu	Glu	Pro	Val
	20				25				30						

Ala	Gly	Ala	Ser	Ile	Ala	Ala	Pro	Leu	Thr	Gly	Gln	Asn	Asn	Val	Ile
	35				40					45					

Asp	Pro	Trp	Ile	Arg	Met	Asn	Phe	Val	Gln	Ala	Pro	Asn	Gly	Glu	Phe
	50				55				60						

Thr	Val	Ser	Pro	Arg	Asn	Ser	Pro	Gly	Glu	Ile	Leu	Leu	Asn	Leu	Glu
	65				70				75				80		

Leu	Gly	Pro	Glu	Leu	Asn	Pro	Phe	Leu	Ala	His	Leu	Ser	Arg	Met	Tyr
	85				90					95					

Asn	Gly	Tyr	Ala	Gly	Gly	Val	Glu	Val	Gln	Val	Leu	Leu	Ala	Gly	Asn
	100				105				110						

Ala	Phe	Thr	Ala	Gly	Lys	Leu	Val	Phe	Ala	Ala	Ile	Pro	Pro	Arg	Phe
	115				120				125						

Pro	Ile	Glu	Asn	Leu	Ser	Pro	Gly	Gln	Ile	Thr	Met	Phe	Pro	His	Val
	130				135				140						

Ile	Ile	Asp	Val	Arg	Thr	Leu	Glu	Pro	Val	Leu	Leu	Pro	Leu	Pro	Asp
	145				150				155				160		

Val	Arg	Asn	Asn	Phe	Phe	His	Tyr	Asn	Gln	Glu	Pro	Gl	Pro	Arg	Met
	165				170				175						

Arg	Leu	Val	Ala	Met	Leu	Tyr	Thr	Pro	Leu	Arg	Ser	Asn	Gly	Ser	Gly
	180				185				190						

Asp	Asp	Val	Phe	Thr	Val	Ser	Cys	Arg	Val	Leu	Thr	Arg	Pro	Ser	Pro
	195				200				205						

Asp	Phe	Asp	Phe	Asn	Tyr	Leu	Val	Pro	Pro	Thr	Val	Glu	Ser	Lys	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-continued

210	215	220
Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Ser Asn Ser		
225	230	235
Arg Phe Pro Ala Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Gly		
245	250	255
Leu Val Val Gln Pro Gln Asn Gly Arg Ser Thr Leu Asp Gly Glu Leu		
260	265	270
Leu Gly Thr Thr Gln Leu Val Pro Ser Asn Ile Cys Ser Leu Arg Gly		
275	280	285
Arg Ile Asn Ala His Leu Pro Asp Asn Gln His Arg Trp Asn Met Gln		
290	295	300
Val Thr Asn Ala Asn Gly Thr Pro Phe Asp Pro Thr Glu Asp Val Pro		
305	310	315
Ala Pro Leu Gly Thr Pro Asp Phe Leu Ala Asn Ile Tyr Gly Val Thr		
325	330	335
Ser Gln Arg Asn Pro Asp Asn Thr Cys Arg Ala His Asp Gly Ile Leu		
340	345	350
Ala Thr Trp Ser Pro Lys Phe Thr Pro Lys Leu Gly Ser Val Val Leu		
355	360	365
Gly Thr Trp Glu Asp Arg Asp Phe Asp Ile Asn Gln Pro Thr Arg Phe		
370	375	380
Thr Pro Val Gly Leu Tyr Asp Thr Asp His Phe Asn Gln Trp Ala Leu		
385	390	395
400		
Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Asn Leu Ala Pro Ser		
405	410	415
Val Ala Pro Leu Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser His		
420	425	430
Ile Pro Leu Lys Gly Gly Thr Ser Asn Gly Ala Ile Asp Cys Leu Leu		
435	440	445
Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Ser		
450	455	460
Thr Asp Val Ala Leu Ile Arg Tyr Thr Asn Pro Asp Thr Gly Arg Val		
465	470	475
480		
Leu Phe Glu Ala Lys Leu His Arg Gln Gly Phe Ile Thr Val Ala Asn		
485	490	495
Ser Gly Ser Arg Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe		
500	505	510
Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly		
515	520	525
Asn Gly Arg Arg Arg Val Gln		
530	535	

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<210> SEQ_ID NO 2
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER_INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(2)
<223> OTHER_INFORMATION: Leu, Val, Asn, Thr, Ser, Met or Arg
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (3)..(3)
<223> OTHER_INFORMATION: Phe, Tyr or Met

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-continued

&lt;400&gt; SEQUENCE: 2

Pro Xaa Xaa Pro Gly Glu  
1 5

```

<210> SEQ_ID NO 3
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER_INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (1)..(1)
<223> OTHER_INFORMATION: Val or Gly
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(2)
<223> OTHER_INFORMATION: Asn or Ser
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (3)..(3)
<223> OTHER_INFORMATION: Gln, Pro or Ser
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(6)
<223> OTHER_INFORMATION: Ser, Thr or Ile
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER_INFORMATION: Ala or Ser
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (10)..(10)
<223> OTHER_INFORMATION: Met or Val

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&lt;400&gt; SEQUENCE: 3

Xaa Xaa Xaa Phe Tyr Xaa Leu Xaa Pro Xaa  
1 5 10

```

<210> SEQ_ID NO 4
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Human norovirus

```

&lt;400&gt; SEQUENCE: 4

Pro Leu Phe Pro Gly Glu  
1 5

```

<210> SEQ_ID NO 5
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Human norovirus

```

&lt;400&gt; SEQUENCE: 5

Pro Val Phe Pro Gly Glu  
1 5

```

<210> SEQ_ID NO 6
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Human norovirus

```

&lt;400&gt; SEQUENCE: 6

Pro Asn Phe Pro Gly Glu  
1 5

```

<210> SEQ_ID NO 7
<211> LENGTH: 6

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<212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 7

Pro Thr Phe Pro Gly Glu  
 1 5

<210> SEQ ID NO 8  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 8

Pro Ser Phe Pro Gly Glu  
 1 5

<210> SEQ ID NO 9  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 9

Pro Thr Tyr Pro Gly Glu  
 1 5

<210> SEQ ID NO 10  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 10

Pro Met Phe Pro Gly Glu  
 1 5

<210> SEQ ID NO 11  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 11

Arg Leu Ser Leu Val Ser  
 1 5

<210> SEQ ID NO 12  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 12

Pro Arg Met Pro Gly Glu  
 1 5

<210> SEQ ID NO 13  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

<400> SEQUENCE: 13

Val Asn Gln Phe Tyr Ser Leu Ala Pro Met  
 1 5 10

<210> SEQ ID NO 14  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus

-continued

&lt;400&gt; SEQUENCE: 14

Val	Asn	Pro	Phe	Tyr	Thr	Leu	Ala	Pro	Met
1			5					10	

&lt;210&gt; SEQ ID NO 15

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 15

Val	Asn	Gln	Phe	Tyr	Thr	Leu	Ala	Pro	Met
1			5					10	

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 16

Val	Asn	Gln	Phe	Tyr	Thr	Leu	Ala	Pro	Val
1			5					10	

&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 17

Val	Asn	Gln	Phe	Tyr	Ser	Leu	Ala	Pro	Met
1			5					10	

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 18

Gly	Asn	Gln	Phe	Tyr	Thr	Leu	Ala	Pro	Met
1			5					10	

&lt;210&gt; SEQ ID NO 19

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 19

Val	Asn	Gln	Phe	Tyr	Ser	Leu	Ala	Pro	Val
1			5					10	

&lt;210&gt; SEQ ID NO 20

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;400&gt; SEQUENCE: 20

Val	Ser	Ser	Phe	Tyr	Ile	Leu	Ser	Pro	Val
1			5					10	

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 542

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: NG1 strain (G2/2)

-continued

&lt;400&gt; SEQUENCE: 21

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala  
 1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val  
 20 25 30

Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile  
 35 40 45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe  
 50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Val Leu Leu Ser Leu Glu  
 65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr  
 85 90 95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn  
 100 105 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe  
 115 120 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val  
 130 135 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp  
 145 150 155 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met  
 165 170 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly  
 180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
 195 200 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr  
 210 215 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser  
 225 230 235 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val  
 245 250 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu  
 260 265 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly  
 275 280 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr  
 290 295 300

Ile Thr Asn Leu Asn Gly Pro Pro Phe Asp Pro Ser Glu Asp Ile Pro  
 305 310 315 320

Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile  
 325 330 335

Ser Gln Arg Asp Lys Gln Asn Ala Ala Gly His Ser Glu Pro Ala Asn  
 340 345 350

Arg Gly His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro  
 355 360 365

Lys Leu Gly Gln Val Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Gln  
 370 375 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Glu  
 385 390 395 400

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu

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405	410	415
Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg		
420	425	430
Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Asn		
435	440	445
Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr		
450	455	460
Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile		
465	470	475
Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala		
485	490	495
Gly Phe Val Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro		
500	505	510
Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser		
515	520	525
Leu Ala Pro Met Gly Ala Gly Asn Gly Arg Arg Arg Val Gln		
530	535	540

&lt;210&gt; SEQ ID NO: 22

&lt;211&gt; LENGTH: 542

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: MK04 strain (G2/2)

&lt;400&gt; SEQUENCE: 22

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala		
1	5	10
		15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val		
20	25	30

Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile		
35	40	45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe		
50	55	60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Val Leu Leu Asn Leu Glu		
65	70	75
		80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr		
85	90	95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn		
100	105	110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe		
115	120	125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val		
130	135	140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp		
145	150	155
		160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met		
165	170	175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly		
180	185	190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro		
195	200	205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr		
210	215	220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser

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225	230	235	240
Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val			
245	250	255	
Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu			
260	265	270	
Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly			
275	280	285	
Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr			
290	295	300	
Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Arg Ser Glu Asp Ile Pro			
305	310	315	320
Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile			
325	330	335	
Ser Gln Arg Asp Lys His Asn Ser Pro Gly His Asn Glu Pro Ala Asn			
340	345	350	
Arg Gly His Asp Ala Val Val Pro Thr Tyr Thr Ser Gln Tyr Thr Pro			
355	360	365	
Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr			
370	375	380	
Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Glu			
385	390	395	400
His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu			
405	410	415	
Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg			
420	425	430	
Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Asn			
435	440	445	
Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr			
450	455	460	
Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile			
465	470	475	480
Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala			
485	490	495	
Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro			
500	505	510	
Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser			
515	520	525	
Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Val Gln			
530	535	540	

&lt;210&gt; SEQ ID NO 23

&lt;211&gt; LENGTH: 548

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: 336 strain (G2/3)

&lt;400&gt; SEQUENCE: 23

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala			
1	5	10	15

Gly Leu Val Pro Glu Ile Asn Asn Glu Ala Met Ala Leu Asp Pro Val		
20	25	30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile		
35	40	45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe

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50	55	60
Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val	Leu Leu Asn Leu Glu	
65	70	75
Leu Gly Pro Glu Ile Asn Pro Tyr Leu Ala His	Leu Ala Arg Met Tyr	
85	90	95
Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val	Val Leu Ala Gly Asn	
100	105	110
Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala	Ile Pro Pro Asn Phe	
115	120	125
Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr	Met Cys Pro His Val	
130	135	140
Ile Val Asp Val Arg Gln Leu Glu Pro Ile Asn	Leu Pro Met Pro Asp	
145	150	155
160		
Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly	Ser Asp Ser Arg Leu	
165	170	175
Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg	Ala Asn Asn Ser Gly	
180	185	190
Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu	Thr Arg Pro Ser Pro	
195	200	205
Asp Phe Ser Phe Asn Phe Leu Val Pro Pro	Thr Val Glu Ser Lys Thr	
210	215	220
Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Ser	Glu Met Ser Asn Ser	
225	230	235
240		
Arg Phe Phe Val Pro Ile Asp Ser Leu His	Thr Ser Pro Thr Glu Ser	
245	250	255
Val Val Val Gln Cys Gln Asn Gly Arg Val	Thr Leu Asp Gly Glu Leu	
260	265	270
Met Gly Thr Thr Gln Leu Leu Pro Ser Gln	Ile Cys Ala Phe Arg Gly	
275	280	285
Thr Leu Thr Arg Pro Thr Asn Arg Ala Ser Asp	Gln Ala Asp Thr Ala	
290	295	300
Thr Pro Arg Leu Phe Asn His Gln Trp His	Ile Gln Leu Asp Asn Leu	
305	310	315
320		
Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp	Ile Pro Ala Pro Leu Gly	
325	330	335
Thr Pro Asp Phe Arg Gly Lys Val Phe Gly	Val Ala Ser Gln Arg Asp	
340	345	350
Pro Asp Gly Thr Thr Arg Ala His Glu Ala Lys	Val Asp Thr Thr Ser	
355	360	365
Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu	Ile Thr Thr Glu Ser	
370	375	380
Asp Asp Phe Asn Gln Asn Lys Pro Thr Arg Phe	Thr Pro Val Gly Ile	
385	390	395
400		
Gly Val Asp Asn Glu Ala Asp Phe Gln Gln	Trp Ile Leu Pro Asp Tyr	
405	410	415
Ser Gly Gln Phe Thr His Asn Met Asn Leu Ala	Pro Ala Val Ala Pro	
420	425	430
Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg	Ser Gln Leu Pro Ser	
435	440	445
Ser Gly Gly Arg Ser Asn Gly Ile Leu Asp Cys	Leu Val Pro Gln Glu	
450	455	460
Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro	Ala Gln Thr Gln Val	
465	470	475
480		

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Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu  
485 490 495

Ala Lys Leu His Lys Met Gly Phe Met Thr Ile Ala Lys Asn Gly Asp  
500 505 510

Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp  
515 520 525

Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Lys Gly Arg  
530 535 540

Arg Arg Ile Gln  
545

<210> SEQ ID NO 24  
<211> LENGTH: 548  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: 18-3 strain (G2/3)

&lt;400&gt; SEQUENCE: 24

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
1 5 10 15

Gly Leu Val Pro Glu Ile Asn Asn Glu Ala Met Ala Leu Glu Pro Val  
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile  
35 40 45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu  
65 70 75 80

Leu Gly Pro Glu Ile Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr  
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn  
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Ile Pro Pro Asn Phe  
115 120 125

Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val  
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Ile Asn Leu Pro Met Pro Asp  
145 150 155 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu  
165 170 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly  
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
195 200 205

Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr  
210 215 220

Lys Leu Phe Thr Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser  
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu His Thr Ser Pro Thr Glu Asn  
245 250 255

Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu  
260 265 270

Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly  
275 280 285

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Thr Leu Thr Arg Pro Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Pro  
 290 295 300  
 Thr Pro Arg Leu Phe Asn His Arg Trp His Ile Gln Leu Asp Asn Leu  
 305 310 315 320  
 Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Ala Pro Leu Gly  
 325 330 335  
 Thr Pro Asp Phe Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn  
 340 345 350  
 Pro Asp Ser Thr Thr Arg Ala His Glu Ala Lys Val Asp Thr Thr Ser  
 355 360 365  
 Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Thr Thr Glu Ser  
 370 375 380  
 Asp Asp Phe Asp Thr Asn Gln Ser Thr Lys Phe Thr Pro Val Gly Ile  
 385 390 395 400  
 Gly Val Asp Asn Glu Ala Glu Phe Gln Gln Trp Ser Leu Pro Asn Tyr  
 405 410 415  
 Ser Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro  
 420 425 430  
 Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser  
 435 440 445  
 Ser Gly Gly Arg Ser Asn Gly Val Leu Asp Cys Leu Val Pro Gln Glu  
 450 455 460  
 Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ala Gln Thr Gln Val  
 465 470 475 480  
 Ala Leu Val Lys Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu  
 485 490 495  
 Ala Lys Leu His Lys Leu Gly Phe Met Thr Ile Ala Lys Asn Gly Asp  
 500 505 510  
 Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp  
 515 520 525  
 Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly Arg  
 530 535 540  
 Arg Arg Ile Gln  
 545

<210> SEQ ID NO 25  
 <211> LENGTH: 549  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus  
 <220> FEATURE:  
 <223> OTHER INFORMATION: 809 strain  
 <400> SEQUENCE: 25  
  
 Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
 1 5 10 15  
  
 Gly Leu Val Pro Glu Ile Asn Asn Glu Ala Met Ala Leu Asp Pro Val  
 20 25 30  
  
 Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile  
 35 40 45  
  
 Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe  
 50 55 60  
  
 Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu  
 65 70 75 80  
  
 Leu Gly Pro Glu Ile Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr  
 85 90 95

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Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn  
     100                        105                        110  
 Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Asn Phe  
     115                        120                        125  
 Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val  
     130                        135                        140  
 Ile Val Asp Val Arg Gln Leu Glu Pro Val Asn Leu Pro Met Pro Asp  
     145                        150                        155                        160  
 Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu  
     165                        170                        175  
 Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly  
     180                        185                        190  
 Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
     195                        200                        205  
 Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr  
     210                        215                        220  
 Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser  
     225                        230                        235                        240  
 Arg Phe Pro Val Pro Ile Glu Ser Leu His Thr Ser Pro Thr Glu Asn  
     245                        250                        255  
 Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu  
     260                        265                        270  
 Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly  
     275                        280                        285  
 Val Leu Thr Arg Ser Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Ala  
     290                        295                        300  
 Thr Pro Arg Leu Phe Asn Tyr Tyr Trp His Val Gln Leu Asp Asn Leu  
     305                        310                        315                        320  
 Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Gly Pro Leu Gly  
     325                        330                        335  
 Thr Pro Asp Pro Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn  
     340                        345                        350  
 Leu Asp Ser Thr Thr Arg Ala His Glu Ala Lys Val Asp Thr Thr Ala  
     355                        360                        365  
 Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Ser Thr Asp Ser  
     370                        375                        380  
 Asp Asp Phe Asp Gln Asn Gln Pro Thr Lys Phe Thr Pro Val Gly Ile  
     385                        390                        395                        400  
 Gly Val Asp Asn Glu Ala Glu Phe Gln Gln Trp Ser Leu Pro Asp Tyr  
     405                        410                        415  
 Ser Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro  
     420                        425                        430  
 Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser  
     435                        440                        445  
 Ser Gly Gly Arg Ser Asn Gly Val Leu Asp Cys Leu Val Pro Gln Glu  
     450                        455                        460  
 Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ala Gln Thr Gln Val  
     465                        470                        475                        480  
 Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Lys Val Leu Phe Glu  
     485                        490                        495  
 Ala Lys Leu His Lys Leu Gly Phe Met Thr Ile Ala Asn Asn Gly Asp  
     500                        505                        510

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Ser Pro Ile Thr Val Pro Pro Ile Asn Gly Tyr Phe Arg Phe Glu Ser  
515 520 525

Trp Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly  
530 535 540

Arg Arg Arg Ile Gln  
545

<210> SEQ\_ID NO 26

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Human norovirus

<220> FEATURE:

<223> OTHER INFORMATION: 104 strain (G2/4)

<400> SEQUENCE: 26

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala  
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val  
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile  
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro  
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr  
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn  
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe  
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile  
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Phe Val Leu Ile Pro Leu Pro Asp  
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Ser Thr Ile  
165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly  
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr  
210 215 220

Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Ser Asn Ser  
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Tyr Thr Gly Pro Ser Ser Ala  
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu  
260 265 270

Leu Gly Thr Thr Gln Leu Ser Ala Val Asn Ile Cys Thr Phe Arg Gly  
275 280 285

Asp Val Thr His Ile Ala Gly Ser His Asp Tyr Thr Met Asn Leu Ala  
290 295 300

Ser Gln Asn Trp Ser Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro  
305 310 315 320

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Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Met Leu Thr Gln  
                   325                  330                  335  
  
 Thr Thr Arg Glu Asp Gly Ser Thr Arg Ala His Lys Ala Thr Val Ser  
                   340                  345                  350  
  
 Thr Gly Ser Val His Phe Thr Pro Lys Leu Gly Ser Val Gln Tyr Thr  
                   355                  360                  365  
  
 Thr Asp Thr Asn Asn Asp Phe Gln Thr Gly Gln Asn Thr Lys Phe Thr  
                   370                  375                  380  
  
 Pro Val Gly Val Ile Gln Asp Gly Asn Asn His Gln Asn Glu Pro Gln  
                   385                  390                  395                  400  
  
 Gln Trp Val Leu Pro Asn Tyr Ser Gly Arg Thr Gly His Asn Val His  
                   405                  410                  415  
  
 Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu Phe  
                   420                  425                  430  
  
 Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asn Leu  
                   435                  440                  445  
  
 Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Cys Gln Glu Ala  
                   450                  455                  460  
  
 Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro Asp  
                   465                  470                  475                  480  
  
 Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr Val  
                   485                  490                  495  
  
 Thr Val Ala His Thr Gly Pro His Asp Leu Val Ile Pro Pro Asn Gly  
                   500                  505                  510  
  
 Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala Pro  
                   515                  520                  525  
  
 Met Gly Asn Gly Ala Gly Arg Arg Ala Leu  
                   530                  535

<210> SEQ\_ID NO 27  
 <211> LENGTH: 540  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus  
 <220> FEATURE:  
 <223> OTHER INFORMATION: 2006a strain (Aomori) (G2/4)

<400> SEQUENCE: 27

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala  
   1              5                  10                  15  
  
 Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val  
   20                  25                  30  
  
 Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile  
   35                  40                  45  
  
 Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Glu Phe  
   50                  55                  60  
  
 Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro  
   65                  70                  75                  80  
  
 Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr  
   85                  90                  95  
  
 Asn Ser Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn  
   100                  105                  110  
  
 Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe  
   115                  120                  125  
  
 Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile  
   130                  135                  140

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Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp  
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile  
165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly  
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr  
210 215 220

Lys Pro Phe Ser Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser  
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala  
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu  
260 265 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly  
275 280 285

Asp Val Thr His Ile Ala Gly Thr Gln Glu Tyr Thr Met Asn Leu Ala  
290 295 300

Ser Gln Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro  
305 310 315 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln  
325 330 335

Thr Thr Arg Arg Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Ser  
340 345 350

Thr Gly Ser Val His Phe Thr Pro Lys Leu Gly Arg Ile Gln Phe Ser  
355 360 365

Thr Asp Thr Ser Asn Asp Phe Glu Thr Gly Gln Asn Thr Arg Phe Thr  
370 375 380

Pro Val Gly Val Val Gln Asp Gly Ser Thr Thr His Gln Asn Glu Pro  
385 390 395 400

Gln Gln Trp Val Leu Pro Asn Tyr Ser Gly Arg Asp Ser His Asn Val  
405 410 415

His Leu Ala Pro Ala Val Ala Pro Ser Phe Pro Gly Glu Gln Leu Leu  
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asn  
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu  
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro  
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr  
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn  
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala  
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu  
530 535 540

<210> SEQ ID NO 28  
<211> LENGTH: 540  
<212> TYPE: PRT

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&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: 2006b strain (Saga) (G2/4)

&lt;400&gt; SEQUENCE: 28

Met	Lys	Met	Ala	Ser	Asn	Asp	Ala	Asn	Pro	Ser	Asp	Gly	Ser	Ala	Ala
1															15
Asn	Leu	Val	Pro	Glu	Val	Asn	Asn	Glu	Val	Met	Ala	Leu	Glu	Pro	Val
	20					25									30
Val	Gly	Ala	Ala	Ile	Ala	Ala	Pro	Val	Ala	Gly	Gln	Gln	Asn	Val	Ile
	35					40									45
Asp	Pro	Trp	Ile	Arg	Asn	Asn	Phe	Val	Gln	Ala	Pro	Gly	Gly	Glu	Phe
	50					55									60
Thr	Val	Ser	Pro	Arg	Asn	Ala	Pro	Gly	Glu	Ile	Leu	Trp	Ser	Ala	Pro
	65					70									80
Leu	Gly	Pro	Asp	Leu	Asn	Pro	Tyr	Leu	Ser	His	Leu	Ala	Arg	Met	Tyr
	85					90									95
Asn	Gly	Tyr	Ala	Gly	Gly	Phe	Glu	Val	Gln	Val	Ile	Leu	Ala	Gly	Asn
	100					105									110
Ala	Phe	Thr	Ala	Gly	Lys	Ile	Ile	Phe	Ala	Ala	Val	Pro	Pro	Asn	Phe
	115					120									125
Pro	Thr	Glu	Gly	Leu	Ser	Pro	Ser	Gln	Val	Thr	Met	Phe	Pro	His	Ile
	130					135									140
Ile	Val	Asp	Val	Arg	Gln	Leu	Glu	Pro	Val	Leu	Ile	Pro	Leu	Pro	Asp
	145					150									160
Val	Arg	Asn	Asn	Phe	Tyr	His	Tyr	Asn	Gln	Ser	Asn	Asp	Ser	Thr	Ile
	165					170									175
Lys	Leu	Ile	Ala	Met	Leu	Tyr	Thr	Pro	Leu	Arg	Ala	Asn	Asn	Ala	Gly
	180					185									190
Glu	Asp	Val	Phe	Thr	Val	Ser	Cys	Arg	Val	Leu	Thr	Arg	Pro	Ser	Pro
	195					200									205
Asp	Phe	Asp	Phe	Ile	Phe	Leu	Val	Pro	Pro	Thr	Val	Glu	Ser	Arg	Thr
	210					215									220
Lys	Pro	Phe	Thr	Val	Pro	Ile	Leu	Thr	Val	Glu	Glu	Met	Thr	Asn	Ser
	225					230									240
Arg	Phe	Pro	Ile	Pro	Leu	Glu	Lys	Leu	Phe	Thr	Gly	Pro	Ser	Gly	Ala
	245					250									255
Phe	Val	Val	Gln	Pro	Gln	Asn	Gly	Arg	Cys	Thr	Thr	Asp	Gly	Val	Leu
	260					265									270
Leu	Gly	Thr	Thr	Gln	Leu	Ser	Pro	Val	Asn	Ile	Cys	Thr	Phe	Arg	Gly
	275					280									285
Asp	Val	Thr	His	Ile	Ala	Gly	Ser	Arg	Asn	Tyr	Thr	Met	Asn	Leu	Ala
	290					295									300
Ser	Leu	Asn	Trp	Asn	Asn	Tyr	Asp	Pro	Thr	Glu	Glu	Ile	Pro	Ala	Pro
	305					310									320
Leu	Gly	Thr	Pro	Asp	Phe	Val	Gly	Lys	Ile	Gln	Gly	Leu	Leu	Thr	Gln
	325					330									335
Thr	Thr	Lys	Gly	Asp	Gly	Ser	Thr	Arg	Gly	His	Lys	Ala	Thr	Val	Tyr
	340					345									350
Thr	Gly	Ser	Ala	Pro	Phe	Thr	Pro	Lys	Leu	Gly	Ser	Val	Gln	Phe	Ser
	355					360									365
Thr	Asp	Thr	Glu	Asn	Asp	Phe	Glu	Thr	His	Gln	Asn	Thr	Lys	Phe	Thr
	370					375									380
Pro	Val	Gly	Val	Ile	Gln	Asp	Gly	Ser	Thr	Thr	His	Arg	Asn	Glu	Pro

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385	390	395	400
Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Val His Asn Val			
405	410	415	
His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu			
420	425	430	
Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp			
435	440	445	
Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu			
450	455	460	
Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro			
465	470	475	480
Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr			
485	490	495	
Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn			
500	505	510	
Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala			
515	520	525	
Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu			
530	535	540	

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 540

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: 2007a strain (G2/4)

&lt;400&gt; SEQUENCE: 29

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala			
1	5	10	15
Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val			
20	25	30	
Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile			
35	40	45	
Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe			
50	55	60	
Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro			
65	70	75	80
Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr			
85	90	95	
Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn			
100	105	110	
Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe			
115	120	125	
Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile			
130	135	140	
Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp			
145	150	155	160
Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile			
165	170	175	
Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly			
180	185	190	
Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro			
195	200	205	
Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr			

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210	215	220
Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser		
225	230	235
Arg Phe Pro Ile Pro Leu Glu Arg Leu Tyr Thr Gly Pro Ser Ser Ala		
245	250	255
Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu		
260	265	270
Leu Gly Thr Thr Gln Leu Ser Ala Val Asn Ile Cys Thr Phe Arg Gly		
275	280	285
Asp Val Thr His Ile Ala Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala		
290	295	300
Ser Gln Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro		
305	310	315
Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Met Leu Thr Gln		
325	330	335
Thr Thr Arg Ser Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Leu		
340	345	350
Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Ala		
355	360	365
Thr Asp Thr Asp Asn Asp Phe Glu Ser Gly Gln Asn Thr Lys Phe Thr		
370	375	380
Pro Val Gly Val Ile Gln Asp Gly Ser Thr Thr His Arg Asn Glu Pro		
385	390	395
Gln Gln Trp Val Leu Pro Asn Tyr Ser Gly Arg Thr Gly His Asn Val		
405	410	415
His Leu Ala Pro Ala Val Ala Pro Thr Tyr Pro Gly Glu Gln Leu Leu		
420	425	430
Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp		
435	440	445
Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu		
450	455	460
Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro		
465	470	475
Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr		
485	490	495
Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn		
500	505	510
Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala		
515	520	525
Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val		
530	535	540

<210> SEQ ID NO 30  
<211> LENGTH: 540  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: 2008a strain (Apeldoorn\_317\_NL\_2007)

&lt;400&gt; SEQUENCE: 30

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala		
1	5	10
15		

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val		
20	25	30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile

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35	40	45
Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe		
50	55	60
Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro		
65	70	75
Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr		
85	90	95
Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn		
100	105	110
Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe		
115	120	125
Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile		
130	135	140
Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp		
145	150	155
Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile		
165	170	175
Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly		
180	185	190
Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro		
195	200	205
Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr		
210	215	220
Lys Pro Phe Ser Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser		
225	230	235
Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala		
245	250	255
Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu		
260	265	270
Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly		
275	280	285
Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala		
290	295	300
Thr Gln Asn Trp Asn Ser Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro		
305	310	315
Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln		
325	330	335
Thr Thr Arg Ala Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr		
340	345	350
Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Ala		
355	360	365
Thr Asp Thr Asp Asn Asp Phe Asp Ala Asn Gln Asn Thr Lys Phe Thr		
370	375	380
Pro Val Gly Val Ile Gln Asp Gly Asn Thr Ala His Arg Asn Glu Pro		
385	390	395
Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Ser His Asn Val		
405	410	415
His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu		
420	425	430
Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp		
435	440	445
Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu		
450	455	460

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Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro  
 465                470                475                480  
 Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr  
 485                490                495  
 Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn  
 500                505                510  
 Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala  
 515                520                525  
 Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu  
 530                535                540

<210> SEQ ID NO 31  
<211> LENGTH: 540  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: 2008a strain (MiyoshiG2-4)

&lt;400&gt; SEQUENCE: 31

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala  
 1                5                10                15  
 Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val  
 20                25                30  
 Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile  
 35                40                45  
 Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe  
 50                55                60  
 Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro  
 65                70                75                80  
 Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr  
 85                90                95  
 Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn  
 100                105                110  
 Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe  
 115                120                125  
 Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile  
 130                135                140  
 Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp  
 145                150                155                160  
 Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Ser Thr Ile  
 165                170                175  
 Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly  
 180                185                190  
 Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
 195                200                205  
 Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr  
 210                215                220  
 Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser  
 225                230                235                240  
 Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala  
 245                250                255  
 Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu  
 260                265                270  
 Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly  
 275                280                285

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Asp Val Ala His Ile Ala Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala  
290 295 300

Pro Leu Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro  
305 310 315 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Met Leu Thr Gln  
325 330 335

Thr Thr Lys Gly Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr  
340 345 350

Thr Gly Ser Ala Asp Phe Thr Pro Lys Leu Gly Ser Val Gln Phe Gly  
355 360 365

Thr Asp Thr Glu Asn Asp Phe Glu Thr His Gln Asn Thr Lys Phe Thr  
370 375 380

Pro Val Gly Val Ile Gln Asp Gly Ser Thr Thr His Arg Asn Glu Pro  
385 390 395 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Val His Asn Val  
405 410 415

His Leu Ala Pro Ala Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu  
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp  
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu  
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro  
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr  
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn  
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala  
515 520 525

Pro Val Gly Asn Gly Thr Gly Arg Arg Arg Val Leu  
530 535 540

<210> SEQ ID NO 32

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Human norovirus

<220> FEATURE:

<223> OTHER INFORMATION: 2009a strain (New)

<400> SEQUENCE: 32

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala  
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val  
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile  
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro  
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr  
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn  
100 105 110

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Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe  
 115 120 125  
 Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile  
 130 135 140  
 Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp  
 145 150 155 160  
 Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile  
 165 170 175  
 Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly  
 180 185 190  
 Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
 195 200 205  
 Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr  
 210 215 220  
 Lys Pro Phe Ser Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser  
 225 230 235 240  
 Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Thr  
 245 250 255  
 Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu  
 260 265 270  
 Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly  
 275 280 285  
 Asp Val Thr His Ile Ala Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala  
 290 295 300  
 Ser Gln Asn Trp Asn Ser Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro  
 305 310 315 320  
 Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln  
 325 330 335  
 Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr  
 340 345 350  
 Thr Gly Ser Ala Asp Phe Ser Pro Lys Leu Gly Arg Val Gln Phe Ala  
 355 360 365  
 Thr Asp Thr Asp Asn Asp Phe Asp Ala Asn Gln Asn Thr Lys Phe Thr  
 370 375 380  
 Pro Val Gly Val Ile Gln Asp Gly Gly Thr Ala His Arg Asn Glu Pro  
 385 390 395 400  
 Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val  
 405 410 415  
 His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu  
 420 425 430  
 Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp  
 435 440 445  
 Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu  
 450 455 460  
 Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro  
 465 470 475 480  
 Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr  
 485 490 495  
 Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn  
 500 505 510  
 Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala  
 515 520 525

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Pro	Met	Gly	Asn
530	535	540	

<210> SEQ ID NO 33  
<211> LENGTH: 540  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: 754 strain (G2/5)

<400> SEQUENCE: 33

Met	Lys	Met	Ala	Ser	Asn	Asp	Ala	Thr	Pro	Ser	Asn	Asp	Gly	Ala	Ala
1				5				10			15				
Gly	Leu	Val	Pro	Glu	Ser	Asn	Asn	Glu	Ala	Met	Ala	Leu	Glu	Pro	Val
	20				25							30			
Val	Gly	Ala	Ser	Leu	Ala	Ala	Pro	Val	Thr	Gly	Gln	Thr	Asn	Ile	Ile
	35					40				45					
Asp	Pro	Trp	Ile	Arg	Thr	Asn	Phe	Val	Gln	Ala	Pro	Asn	Gly	Glu	Phe
	50					55				60					
Thr	Val	Ser	Pro	Arg	Asn	Ser	Pro	Gly	Glu	Ile	Leu	Val	Asn	Leu	Glu
	65				70				75			80			
Leu	Gly	Pro	Glu	Leu	Asn	Pro	Tyr	Leu	Ala	His	Leu	Ala	Arg	Met	Tyr
	85					90							95		
Asn	Gly	Tyr	Ala	Gly	Gly	Met	Glu	Val	Gln	Val	Met	Leu	Ala	Gly	Asn
	100					105					110				
Ala	Phe	Thr	Ala	Gly	Lys	Ile	Ile	Phe	Ala	Ala	Val	Pro	Pro	Tyr	Phe
	115					120					125				
Pro	Val	Glu	Asn	Leu	Ser	Pro	Ser	Gln	Ile	Thr	Met	Phe	Pro	His	Val
	130					135				140					
Ile	Ile	Asp	Val	Arg	Thr	Leu	Glu	Pro	Val	Leu	Leu	Pro	Met	Pro	Asp
	145					150				155			160		
Val	Arg	Ser	Thr	Leu	Phe	His	Phe	Asn	Gln	Lys	Asp	Glu	Pro	Lys	Met
	165					170				175					
Arg	Leu	Val	Ala	Met	Leu	Tyr	Thr	Pro	Leu	Arg	Ser	Asn	Gly	Ser	Gly
	180					185				190					
Asp	Asp	Val	Phe	Thr	Val	Ser	Cys	Arg	Ile	Leu	Thr	Arg	Pro	Ser	Pro
	195					200				205					
Glu	Phe	Asp	Phe	Thr	Tyr	Leu	Val	Pro	Pro	Thr	Val	Glu	Ser	Lys	Thr
	210					215				220					
Lys	Pro	Phe	Thr	Leu	Pro	Val	Leu	Thr	Leu	Gly	Glu	Leu	Ser	Asn	Ser
	225					230				235			240		
Arg	Phe	Pro	Leu	Ser	Ile	Asp	Glu	Met	Val	Thr	Ser	Pro	Asn	Glu	Ser
	245					250				255					
Ile	Val	Val	Gln	Pro	Gln	Asn	Gly	Arg	Val	Thr	Leu	Asp	Gly	Glu	Leu
	260					265				270					
Leu	Gly	Thr	Thr	Gln	Leu	Gln	Ala	Cys	Asn	Ile	Cys	Ser	Ile	Arg	Gly
	275					280				285					
Lys	Val	Thr	Gly	Gln	Val	Pro	Ser	Glu	Gln	His	Met	Trp	Asn	Leu	Glu
	290					295				300					
Ile	Thr	Asn	Leu	Asn	Gly	Thr	Gln	Phe	Asp	Pro	Thr	Asp	Asp	Val	Pro
	305					310				315			320		
Ala	Pro	Leu	Gly	Val	Pro	Asp	Phe	Ala	Gly	Glu	Val	Phe	Gly	Val	Leu
	325					330				335			340		
Ser	Gln	Arg	Asn	Arg	Gly	Glu	Ser	Asn	Pro	Ala	Asn	Arg	Ala	His	Asp
	340					345				350					

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Ala Val Val Ala Thr Tyr Ser Asp Lys Tyr Thr Pro Lys Leu Gly Leu  
 355 360 365  
 Val Gln Ile Gly Thr Trp Asn Thr Asn Asp Val Glu Asn Gln Pro Thr  
 370 375 380  
 Lys Phe Thr Pro Ile Gly Leu Asn Glu Val Ala Asn Gly His Arg Phe  
 385 390 395 400  
 Glu Gln Trp Thr Leu Pro Arg Tyr Ser Gly Ala Leu Thr Leu Asn Met  
 405 410 415  
 Asn Leu Ala Pro Ala Val Ala Pro Leu Phe Pro Gly Glu Arg Leu Leu  
 420 425 430  
 Phe Phe Arg Ser Tyr Val Pro Leu Lys Gly Gly Phe Gly Asn Pro Ala  
 435 440 445  
 Ile Asp Cys Ser Val Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu  
 450 455 460  
 Ser Ala Pro Ser Leu Gly Asp Val Ala Leu Val Arg Tyr Val Asn Pro  
 465 470 475 480  
 Asp Thr Gly Arg Val Leu Phe Glu Ala Lys Leu His Lys Gly Gly Phe  
 485 490 495  
 Leu Thr Val Ser Ser Thr Ser Thr Gly Pro Val Val Val Pro Ala Asn  
 500 505 510  
 Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala  
 515 520 525  
 Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Val Gln  
 530 535 540

<210> SEQ\_ID NO 34  
 <211> LENGTH: 550  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus  
 <220> FEATURE:  
 <221> NAME/KEY: MOD\_RES  
 <222> LOCATION: (550) ..(550)  
 <223> OTHER INFORMATION: Any amino acid  
 <220> FEATURE:  
 <223> OTHER INFORMATION: 445 strain (G2/6)

<400> SEQUENCE: 34

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
 1 5 10 15  
 Asn Leu Val Pro Glu Ala Asn Asn Glu Val Met Ala Leu Glu Pro Val  
 20 25 30  
 Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile  
 35 40 45  
 Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe  
 50 55 60  
 Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Glu  
 65 70 75 80  
 Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ser His Leu Ser Arg Met Tyr  
 85 90 95  
 Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn  
 100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe  
 115 120 125  
 Pro Val Asp Asn Ile Ser Ala Ala Gln Ile Thr Met Cys Pro His Val  
 130 135 140  
 Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp  
 145 150 155 160

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Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Pro Arg Met  
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu  
180 185 190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp  
195 200 205

Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys  
210 215 220

Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg  
225 230 235 240

Phe Pro Ala Ala Ile Asp Met Leu Tyr Ala Asp Pro Asn Glu Ser Ile  
245 250 255

Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln  
260 265 270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr  
275 280 285

Leu Ile Ser Gln Thr Ala Arg Ala Thr Asp Ser Thr Asp Ser Pro Gln  
290 295 300

Arg Ala Arg Asp His Pro Leu His Val Gln Val Lys Asn Leu Asp Gly  
305 310 315 320

Thr Gln Tyr Asp Pro Thr Asp Asp Ile Pro Ala Val Leu Gly Ala Ile  
325 330 335

Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser  
340 345 350

Gly Pro Gln Glu Gln Gly His Tyr Ala Thr Arg Ala His Glu Ala His  
355 360 365

Ile Asp Thr Thr Asp Pro Lys Tyr Ala Pro Lys Leu Gly Thr Ile Leu  
370 375 380

Ile Lys Ser Glu Ser Asn Asp Phe Ile Thr Asn Gln Pro Ile Arg Phe  
385 390 395 400

Thr Pro Val Gly Met Gly Asp Asn Asn Trp Arg Gln Trp Glu Leu Pro  
405 410 415

Asp Tyr Ser Gly Arg Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val  
420 425 430

Ser Pro Ser Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val  
435 440 445

Pro Ser Ala Gly Gly Tyr Gly Ser Gly Tyr Ile Asp Cys Leu Ile Pro  
450 455 460

Gln Glu Trp Gly Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser  
465 470 475 480

Ala Val Ala Leu Val Arg Tyr Tyr Asn Pro Asp Thr Gly Arg Asn Ile  
485 490 495

Phe Glu Ala Lys Leu His Arg Glu Gly Phe Leu Thr Val Ala Asn Ser  
500 505 510

Gly Asn Asn Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu  
515 520 525

Ala Trp Val Asn Gln Phe Tyr Thr Leu Ala Pro Met Gly Ser Gly Gln  
530 535 540

Gly Arg Arg Arg Ala Xaa  
545 550

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<212> TYPE: PRT  
 <213> ORGANISM: Human norovirus  
 <220> FEATURE:  
 <223> OTHER INFORMATION: 7k strain (G2/6)

<400> SEQUENCE: 35

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1           5           10          15

Asn Leu Val Pro Glu Ala Asn Asp Glu Val Met Ala Leu Glu Pro Val
20          25          30

Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
35          40          45

Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe
50          55          60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Glu
65          70          75          80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ser His Leu Ser Arg Met Tyr
85          90          95

Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn
100         105         110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe
115         120         125

Pro Val Glu Asn Ile Ser Ala Ala Gln Ile Thr Met Cys Pro His Val
130         135         140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145         150         155         160

Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Pro Arg Met
165         170         175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu
180         185         190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp
195         200         205

Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys
210         215         220

Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg
225         230         235         240

Phe Pro Ala Ala Ile Asp Met Leu Tyr Thr Asp Pro Asn Glu Ser Ile
245         250         255

Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln
260         265         270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr
275         280         285

Leu Ile Ser Gln Thr Ala Arg Ala Ala Asp Ser Thr Asp Ser Pro Gln
290         295         300

Arg Ala Arg Asn His Pro Leu His Val Gln Val Lys Asn Leu Asp Gly
305         310         315         320

Thr Gln Tyr Asp Pro Thr Asp Asp Ile Pro Ala Val Leu Gly Ala Ile
325         330         335

Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser
340         345         350

Gly Gln Gln Glu Gln Gly His Tyr Ala Thr Arg Ala His Glu Ala His
355         360         365

Ile Asp Thr Thr Asp Pro Lys Tyr Ala Pro Lys Leu Gly Thr Ile Leu
370         375         380

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Ile Lys Ser Gly Ser Asp Asp Phe Asn Thr Asn Gln Pro Ile Arg Phe  
385 390 395 400

Thr Pro Val Gly Met Gly Asp Asn Asn Trp Arg Gln Trp Glu Leu Pro  
405 410 415

Asp Tyr Ser Gly Arg Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val  
420 425 430

Ser Pro Ser Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val  
435 440 445

Pro Ser Ala Gly Gly Tyr Gly Ser Gly Tyr Ile Asp Cys Leu Ile Pro  
450 455 460

Gln Glu Trp Val Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser  
465 470 475 480

Ala Val Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Asn Ile  
485 490 495

Phe Glu Ala Lys Leu His Arg Glu Gly Phe Leu Thr Val Ala Asn Cys  
500 505 510

Gly Asn Asn Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu  
515 520 525

Ala Trp Gly Asn Gln Phe Tyr Thr Leu Ala Pro Met Gly Ser Gly Gln  
530 535 540

Gly Arg Arg Arg Ala Gln  
545 550

<210> SEQ ID NO 36  
<211> LENGTH: 537  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: U25 strain (G2/8)

&lt;400&gt; SEQUENCE: 36

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
1 5 10 15

Gly Leu Val Pro Glu Ile Asn His Glu Val Met Ala Ile Glu Pro Val  
20 25 30

Ala Gly Ala Ser Leu Ala Ala Pro Val Val Gly Gln Leu Asn Ile Ile  
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Ala Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Phe Leu Leu Asp Leu Glu  
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr  
85 90 95

Asn Gly His Ala Gly Gly Met Glu Val Gln Ile Val Leu Ala Gly Asn  
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Val Ile Pro Pro Gly Phe  
115 120 125

Pro Tyr Glu Asn Leu Ser Pro Ala Gln Leu Thr Met Cys Pro His Val  
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Ile Leu Leu Pro Met Pro Asp  
145 150 155 160

Ile Arg Asn Thr Phe Phe His Tyr Asn Gln Ser Asn Gly Pro Lys Leu  
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly  
180 185 190

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Glu Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
195 200 205

Asp Phe Glu Phe Asn Phe Leu Val Pro Pro Ser Val Glu Ser Lys Thr  
210 215 220

Lys Ala Phe Thr Leu Pro Ile Leu Lys Ile Ser Glu Met Thr Asn Ser  
225 230 235 240

Arg Phe Pro Ile Pro Val Asp Gln Met Tyr Thr Ser Arg Asn Glu Asn  
245 250 255

Ile Val Val Gln Pro Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu  
260 265 270

Gln Gly Thr Thr Thr Leu Gln Pro Val Ser Ile Cys Gly Phe Arg Gly  
275 280 285

Thr Leu Gln Thr Arg Leu Ala Asp Gln Pro Asn Tyr Thr Tyr Gln Val  
290 295 300

His Leu Glu Asn Leu Asp Gly Ser Pro Val Asp Pro Thr Asp Glu Val  
305 310 315 320

Pro Ala Pro Leu Gly Thr Pro Asp Phe Gln Ala Gln Leu Phe Gly Val  
325 330 335

Ile Ser Gln Arg Ser Ser Asp Asn Ala Thr Arg Ala His Glu Ala Arg  
340 345 350

Val Asn Thr Asn Asp Pro Thr Phe Ala Pro Gln Ile Ala Gln Val Arg  
355 360 365

Phe Lys Ser Pro Ser Asn Asp Phe Phe Asp Asn Glu Pro Ile Lys Phe  
370 375 380

Thr Pro Val Gly Ile Ser Val Asp Ser Gln Asn Ser Tyr Asn Gln Trp  
385 390 395 400

Leu Leu Pro Arg Tyr Gly His Leu Thr Asn Asn Thr His Leu Ala  
405 410 415

Pro Ser Val Ser Pro Met Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg  
420 425 430

Ser Phe Met Pro Gly Ala Ser Gly His Thr Asp Gly Ala Ile Asp Cys  
435 440 445

Leu Leu Pro Gln Glu Trp Val Ala His Phe Tyr Gln Glu Ala Ala Thr  
450 455 460

Ala Gln Thr Asp Val Ala Leu Ile Arg Phe Val Asn Pro Asp Thr Gly  
465 470 475 480

Arg Val Leu Phe Glu Gly Lys Leu His Lys Gln Gly Phe Ile Thr Ile  
485 490 495

Ser Asn Ser Gly Asp His Pro Ile Val Met Pro Ala Asn Gly Tyr Phe  
500 505 510

Arg Phe Glu Ala Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Val Gly  
515 520 525

Thr Gly Ser Gly Arg Arg Ile Gln  
530 535

<210> SEQ ID NO 37  
<211> LENGTH: 548  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: Viet026 strain (G2/10)

<400> SEQUENCE: 37

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
1 5 10 15

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Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val  
20 25 30

Ala Gly Ala Ser Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile  
35 40 45

Asp Pro Trp Ile Arg Met Asn Phe Val Gln Ala Pro Asn Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu  
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr  
85 90 95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Ile Met Leu Ala Gly Asn  
100 105 110

Ala Phe Thr Ala Gly Lys Leu Ile Phe Ala Ala Val Pro Pro His Phe  
115 120 125

Pro Ile Glu Asn Leu Ser Pro Pro Gln Ile Thr Met Phe Pro His Val  
130 135 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Met Pro Asp  
145 150 155 160

Ile Arg Asn Ser Phe Phe His Phe Ile Gln Arg Asp Glu Pro Lys Met  
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly  
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro  
195 200 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Ser  
210 215 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Thr Asn Ser  
225 230 235 240

Arg Phe Pro Leu Pro Ile Asp Val Leu Tyr Thr Asn Pro Asn Glu Ser  
245 250 255

Ala Ile Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu  
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Thr Gly Ile Cys Ala Phe Arg Gly  
275 280 285

Lys Val Thr Gln Gln Val Gln Asp Glu His Arg Gly Thr His Trp Asn  
290 295 300

Met Thr Val Thr Asn Leu Asn Gly Thr Pro Phe Asp Pro Thr Glu Asp  
305 310 315 320

Val Pro Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Gln Ile Tyr Gly  
325 330 335

Val Ile Ser Gln Arg Asn Thr Asn Thr Val Pro Gly Glu Gly Asn Leu  
340 345 350

Pro Ala Asn Arg Ala His Glu Ala Val Ile Ala Thr Tyr Ser Pro Lys  
355 360 365

Phe Thr Pro Lys Leu Gly Asn Ile Gln Phe Ser Thr Trp Glu Thr Gln  
370 375 380

Asp Val Ser Ser Gly Gln Pro Thr Lys Phe Thr Pro Val Gly Leu Ala  
385 390 395 400

Ser Val Asp Ala Asn Ser His Phe Asp Gln Trp Thr Leu Pro Ser Tyr  
405 410 415

Ser Gly Ala Leu Thr Leu Asn Met Asn Leu Ala Pro Ser Val Ala Pro  
420 425 430

Val Phe Pro Gly Glu Cys Leu Leu Phe Phe Arg Ser Phe Ile Pro Leu

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435	440	445
Lys Gly Gly Tyr Gly Asn Pro Ala Ile Asp Cys Leu Met Pro Gln Glu		
450	455	460
Trp Val Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Leu Ser Asp Val		
465	470	475
Ala Leu Val Arg Tyr Val Asn Pro Glu Thr Gly Arg Thr Leu Phe Glu		
485	490	495
Ala Lys Leu His Arg Asn Gly Phe Leu Thr Val Ala Arg Asn Ser Ala		
500	505	510
Gly Pro Val Val Ala Pro Thr Asn Gly Tyr Phe Arg Phe Asp Ser Trp		
515	520	525
Val Asn Gln Phe Tyr Thr Leu Ala Pro Met Gly Asn Gly Ser Gly Arg		
530	535	540
Arg Arg Met Gln		
545		

<210> SEQ ID NO 38  
<211> LENGTH: 535  
<212> TYPE: PRT  
<213> ORGANISM: Human norovirus  
<220> FEATURE:  
<223> OTHER INFORMATION: 76 strain (G2/12)

<400> SEQUENCE: 38

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala		
1	5	10
15		
Gly Leu Val Pro Glu Ala Asn Asn Glu Thr Met Ala Leu Glu Pro Val		
20	25	30
30		
Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Ile Ile		
35	40	45
45		
Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe		
50	55	60
60		
Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu		
65	70	75
75		
80		
Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr		
85	90	95
95		
Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn		
100	105	110
110		
Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe		
115	120	125
125		
Pro Leu Glu Asn Ile Ser Pro Gly Gln Ile Thr Met Phe Pro His Val		
130	135	140
140		
Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp		
145	150	155
155		
160		
Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Asn Glu Pro Arg Met		
165	170	175
175		
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly		
180	185	190
190		
Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro		
195	200	205
205		
Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Leu Glu Ser Lys Thr		
210	215	220
220		
Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser		
225	230	235
235		
240		
Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Ser		

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245	250	255
Leu Val Val Gln Pro Gln Asn Gly Arg Cys Ala Leu Asp Gly Glu Leu		
260	265	270
Gln Gly Thr Thr Gln Leu Leu Pro Thr Ala Ile Cys Ser Phe Arg Gly		
275	280	285
Arg Ile Asn Gln Lys Val Ser Gly Glu Asn His Val Trp Asn Met Gln		
290	295	300
Val Thr Asn Ile Asn Gly Thr Pro Phe Asp Pro Thr Gly Asp Val Pro		
305	310	315
Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Lys Leu Phe Gly Val Leu		
325	330	335
Ser Gln Arg Asp His Asp Asn Ala Cys Arg Ser His Asp Ala Val Ile		
340	345	350
Ala Thr Asn Ser Ala Lys Phe Thr Pro Lys Leu Gly Ala Ile Gln Ile		
355	360	365
Gly Thr Trp Glu Glu Asp Asp Val His Ile Asn Gln Pro Thr Lys Phe		
370	375	380
Thr Pro Val Gly Leu Phe Glu Asn Glu Gly Phe Asn Gln Trp Thr Leu		
385	390	395
Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Gly Leu Ala Pro Pro		
405	410	415
Val Ala Pro Thr Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His		
420	425	430
Ile Pro Leu Lys Gly Gly Val Ala Asp Pro Val Ile Asp Cys Leu Leu		
435	440	445
Pro Gln Glu Trp Ile Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Gln		
450	455	460
Ser Asp Val Ala Leu Ile Arg Phe Thr Asn Pro Asp Thr Gly Arg Val		
465	470	475
Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr Val Ala Asn		
485	490	495
Thr Gly Ser Arg Pro Ile Val Val Pro Ala Asn Gly Tyr Phe Arg Phe		
500	505	510
Asp Thr Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly		
515	520	525
Asn Gly Arg Arg Val Gln		
530	535	

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 542

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Human norovirus

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: 47 strain (G2/14)

&lt;400&gt; SEQUENCE: 39

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala		
1	5	10
15		
Ser Leu Val Pro Glu Gly Ile Asn Glu Thr Met Pro Leu Glu Pro Val		
20	25	30
30		
Ala Gly Ala Ser Ile Ala Ala Pro Val Ala Gly Gln Thr Asn Ile Ile		
35	40	45
45		
Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe		
50	55	60
60		
Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu		

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65	70	75	80
Leu	Gly	Pro	Asp
Leu	Asn	Pro	Tyr
85	90	95	
Leu	Ser	Arg	Met
			Tyr
Asn	Gly	Tyr	Ala
100	105	110	Gly
Ala	Gly	Gly	Val
115	120	125	Glu
Phe	Thr	Ala	Gly
130	135	140	Lys
Ile	Leu	Phe	Ala
145	150	155	Ala
Ile	Pro	Pro	Asn
160			Phe
Val	Asp	Val	Arg
165	170	175	Thr
Leu	Glu	Pro	Ile
180	185	190	Met
Arg	Leu	Pro	Leu
195	200	205	Arg
Asp	Phe	Thr	Val
210	215	220	Ser
Cys	Arg	Val	Leu
225	230	235	Thr
Leu	Thr	Ile	Asn
240			Ser
Pro	Phe	Leu	Glu
245	250	255	Leu
Ile	Glu	Pro	Asn
260	265	270	Gly
Asn	Val	Val	Gln
275	280	285	Cys
Gln	Gly	Thr	Gln
290	295	300	Leu
Arg	Thr	Val	Ala
305	310	315	Asp
Asn	Gly	Asp	Asn
320			Trp
Leu	Thr	Tyr	Asp
325	330	335	Pro
Pro	Asn	Asn	Glu
340	345	350	Val
Asp	Asn	Val	Leu
355	360	365	Ser
Gly	Ile	Tyr	Ile
370	375	380	Ser
Ser	Ile	Gly	Leu
385	390	395	His
Arg	Phe	Thr	Ile
395			Thr
Ser	Val	Gly	Asp
405	410	415	Ala
Gln	Gln	Trp	Asn
420	425	430	Gly
Asn	Leu	Ala	Val
435	440	445	Ala
Leu	Pro	Ala	Arg
450	455	460	Leu
Ala	Phe	Ile	Asp
465	470	475	Cys
Glu	Ala	Ala	Pro
485	490	495	Ser
Gln	Asp	Thr	Gly
495			Arg
Asn	Pro	Asp	Thr
500			Gly
Leu	Phe	Leu	Leu
505	510	515	Asp
Ala	Gly	Ala	Asp
520	525	530	Val
Leu	Leu	Ile	Leu
535	540	545	Arg
Ile	Arg	Tyr	Tyr
550	555	560	Val

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Gly Phe Ile Thr Val Ser His Thr Gly Ala Tyr Pro Leu Val Val Pro  
500 505 510

Pro Asn Gly His Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser  
515 520 525

Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln  
530 535 540

<210> SEQ ID NO 40

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Human norovirus

<220> FEATURE:

<223> OTHER INFORMATION: Kamo8 strain (G2/15)

<400> SEQUENCE: 40

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala  
1 5 10 15

Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val  
20 25 30

Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile  
35 40 45

Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe  
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu  
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr  
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn  
100 105 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Ile Pro Pro His Phe  
115 120 125

Pro Val Asp Asn Leu Ser Pro Gly Gln Ile Thr Met Phe Pro His Val  
130 135 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp  
145 150 155 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Ser Asp Gln Arg Met  
165 170 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly  
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro  
195 200 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr  
210 215 220

Lys Pro Phe Ser Val Pro Val Leu Thr Leu Asn Glu Leu Thr Asn Ser  
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ala Met Tyr Thr Ser Pro Asn Asp Ser  
245 250 255

Ile Val Val Gln Pro Gln Asn Gly Arg Ala Thr Ile Asp Gly Glu Leu  
260 265 270

Leu Gly Thr Thr Gln Leu Ile Pro Ser Gly Ile Cys Ser Phe Arg Gly  
275 280 285

Lys Ile Thr Thr His Leu Ala Asp Asp Arg His Leu Trp Asn Ile Gln  
290 295 300

Val Ser Asn Leu Asn Gly Thr Pro Phe Asp Pro Thr Asp Asp Val Pro  
305 310 315 320

-continued

Ala Pro Leu Gly Met Pro Asp Phe Ser Gly Gln Ile Phe Gly Val Val  
                   325                  330                  335  
 Ser Gln Arg Asp Thr Gly Thr Asn Pro Ala Asn Arg Ala His Asp Ala  
                   340                  345                  350  
 Val Leu Ala Thr Tyr Ser Ala Lys Tyr Thr Pro Lys Leu Gly Ser Val  
                   355                  360                  365  
 Gln Ile Gly Thr Trp Asp Thr Glu Asp Leu Leu Glu Arg Gln Pro Val  
                   370                  375                  380  
 Lys Phe Thr Pro Val Gly Leu Asn Glu Ile Gly Gln Asp Lys His Phe  
                   385                  390                  395                  400  
 Asp Gln Trp Val Leu Pro Asn Tyr Ser Gly Ala Leu Gly Leu Asn Met  
                   405                  410                  415  
 His Leu Ala Pro Ala Val Ser Pro Leu Phe Pro Gly Glu Arg Leu Leu  
                   420                  425                  430  
 Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly His Gly Asp Pro Phe  
                   435                  440                  445  
 Ile Asp Cys Leu Val Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu  
                   450                  455                  460  
 Ser Ala Pro Ala Gln Ser Ser Val Ala Leu Leu Arg Tyr Val Asn Pro  
                   465                  470                  475                  480  
 Asp Thr Gly Arg Thr Leu Phe Glu Ala Lys Leu His Lys Glu Gly Phe  
                   485                  490                  495  
 Ile Thr Val Ser Ser Thr Glu Asn Arg Pro Val Ile Val Pro Pro Asn  
                   500                  505                  510  
 Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala  
                   515                  520                  525  
 Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Val Gln  
                   530                  535                  540

<210> SEQ ID NO 41  
 <211> LENGTH: 556  
 <212> TYPE: PRT  
 <213> ORGANISM: Human norovirus  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Alpha23 strain (G2/17)

<400> SEQUENCE: 41

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Gly  
   1              5                  10                  15  
 Asn Leu Val Pro Glu Ser Gln Gln Glu Val Leu Pro Leu Ala Pro Val  
   20              25                  30  
 Ala Gly Ala Ala Leu Ala Ala Pro Val Val Gly Gln Thr Asn Ile Ile  
   35              40                  45  
 Asp Pro Trp Ile Lys Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe  
   50              55                  60  
 Thr Val Ser Pro Lys Asn Ser Pro Gly Glu Ile Leu Val Asn Leu Glu  
   65              70                  75                  80  
 Leu Gly Pro Lys Leu Asn Pro Tyr Leu Asp His Leu Ser Arg Met Tyr  
   85              90                  95  
 Asn Ser Tyr Ala Gly Gly Ile Asp Val Met Val Val Leu Ala Gly Asn  
   100            105                  110  
 Ala Phe Thr Ala Gly Lys Val Leu Ile Ala Ala Ile Pro Pro Asn Phe  
   115            120                  125  
 Pro Val Glu Gly Val Ser Ala Ser Gln Ala Thr Gln Phe Pro His Val  
   130            135                  140

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Ile Ile Asp Val Arg Thr Leu Asp Pro Val Arg Leu Pro Leu Pro Asp  
145 150 155 160

Val Arg Ser Thr Phe Phe His Tyr Thr Asn Asp Thr Glu Pro Lys Met  
165 170 175

Arg Leu Val Ile Trp Leu Tyr Thr Pro Leu Arg Thr Asn Gly Ser Gly  
180 185 190

Asp Asp Ser Phe Thr Val Ser Gly Arg Ile Leu Thr Arg Pro Ser Gln  
195 200 205

Asp Phe Glu Phe Ala Phe Leu Ile Pro Pro Thr Val Glu Thr Lys Thr  
210 215 220

Thr Pro Phe Ser Val Pro Gly Phe Ser Val Gln Glu Met Ser Asn Ser  
225 230 235 240

Arg Trp Pro Ala Ala Ile Ser Ala Met Val Val Arg Gly Asn Glu Pro  
245 250 255

Gln Val Val Gln Phe Gln Asn Gly Arg Ala His Leu Asp Gly Met Leu  
260 265 270

Leu Gly Thr Thr Pro Val Ser Pro Asn Tyr Ile Ala Ser Tyr Arg Gly  
275 280 285

Ile Ser Thr Gly Asn Ser Arg Ser Ala Ser Ser Glu Ala Asp Glu Arg  
290 295 300

Ala Val Gly Ser Phe Asp Val Trp Val Arg Leu Gln Glu Pro Asp Gly  
305 310 315 320

Gln Pro Tyr Asp Ile Phe Gly Lys Gln Pro Ala Pro Ile Gly Thr Pro  
325 330 335

Asp Phe Lys Ala Val Ile Val Gly Phe Ala Ala Arg Pro Leu Thr Ser  
340 345 350

Gly Ser Tyr Ala Asn Glu Ala Tyr Val Asn Thr Thr Ala Ser Asp Tyr  
355 360 365

Ala Pro Ala Thr Gly Asn Met Arg Phe Thr Val Arg Asn Gly Thr  
370 375 380

Gly His Ile Ser Ala Asn Lys Tyr Trp Glu Phe Lys Ser Phe Gly Val  
385 390 395 400

Glu Gly Glu Arg His Thr Asn Ile Gln Tyr Gln Glu Tyr Glu Leu Pro  
405 410 415

Asp Tyr Ser Gly Gln Val Ala Ser Asn His Asn Leu Ala Pro Pro Val  
420 425 430

Ala Pro Arg Met Pro Gly Glu Ser Leu Leu Leu Phe Gln Ser Ser Met  
435 440 445

Pro Val Trp Asp Asp Gly His Gly Glu Ser Thr Pro Lys Lys Ile His  
450 455 460

Cys Leu Leu Pro Gln Glu Phe Ile Gly His Phe Phe Asp Lys Gln Ala  
465 470 475 480

Pro Ser Leu Gly Asp Ala Ala Leu Leu Arg Tyr Val Asn Gln Glu Thr  
485 490 495

Asn Arg Val Leu Phe Glu Cys Lys Leu Tyr Arg Asp Gly Tyr Ile Thr  
500 505 510

Val Ala Ala Ser Ser Gly Leu Leu Asp Phe Pro Leu Asp Gly Phe Phe  
515 520 525

Arg Phe Asp Ser Trp Val Ser Ser Phe Tyr Ile Leu Ser Pro Val Gly  
530 535 540

Ser Gly Gln Gly Arg Arg Gly Arg Val Arg Phe Gln  
545 550 555

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The invention claimed is:

1. An anti-human-norovirus GII antibody that binds to epitopes in an amino acid region represented by (i), (ii), and (iii):

(i) an epitope in an amino acid region of at least one amino acid sequence of formula (1):

P-X<sup>1</sup>-X<sup>2</sup>-P-G-E

(1) (SEQ ID NO: 2)

wherein

X<sup>1</sup> represents L, V, N, T, S, M, or R;

X<sup>2</sup> represents F, Y, S or M;

(ii) an epitope in an amino acid region of at least one amino acid sequence of formula (2)

X<sup>3</sup>-X<sup>4</sup>-X<sup>5</sup>-F-Y-X<sup>6</sup>-L-X<sup>7</sup>-P-X<sup>8</sup>

(2) (SEQ ID NO: 3)

wherein

X<sup>3</sup> represents V or G;

X<sup>4</sup> represents N or S;

X<sup>5</sup> represents Q, P, or S;

X<sup>6</sup> represents S, T, or I;

X<sup>7</sup> represents A or S; and

X<sup>8</sup> represents M or V; and

(iii) an epitope in an amino acid region comprising amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1, or comprising an amino acid corresponding to amino acid 483 of the amino acid sequence represented by SEQ ID NO: 1,

wherein the amino acid region represented by (i), (ii), and (iii) is present in a P domain of a capsid structural protein of a human norovirus GII.

2. The anti-human-norovirus GII antibody according to claim 1, wherein the amino acid region represented by formula (1) is a region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1, and the amino acid region represented by formula (2) is a region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1.

3. A human norovirus GII detection reagent comprising the antibody of claim 1.

4. A method for detecting a human norovirus GII, the method comprising reacting a specimen suspected to contain the human norovirus GII with the antibody of claim 1, and performing an immunological assay to detect the virus.

5. A human norovirus GII detection reagent comprising the antibody of claim 2.

6. A method for detecting a human norovirus GII, the method comprising reacting a specimen suspected to contain the human norovirus GII with the antibody of claim 2, and performing an immunological assay to detect the virus.

7. The anti-human-norovirus GII antibody of claim 1, wherein the amino acid region represented by formula (1) is a region from amino acid 419 to amino acid 424 of the amino acid sequence represented by SEQ ID NO: 1.

8. The anti-human-norovirus GII antibody of claim 1, wherein the amino acid region represented by formula (2) is a region from amino acid 516 to amino acid 525 of the amino acid sequence represented by SEQ ID NO: 1.

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9. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>2</sup> in the amino acid sequence of formula (1) is F.

10. The anti-human-norovirus GII antibody according to claim 1, wherein the amino acid sequence of formula (1) is selected from the group consisting of:

P-L-F-P-G-E (1-1)(SEQ ID NO: 4),

P-V-F-P-G-E (1-2) (SEQ ID NO: 5),

P-N-F-P-G-E (1-3) (SEQ ID NO: 6),

P-T-F-P-G-E (1-4) (SEQ ID NO: 7),

P-S-F-P-G-E (1-5) (SEQ ID NO: 8),

P-T-Y-P-G-E (1-6) (SEQ ID NO: 9),

P-M-F-P-G-E (1-7) (SEQ ID NO: 10),

P-R-M-P-G-E (1-9) (SEQ ID NO: 12).

11. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>3</sup> in the amino acid sequence of formula (2) is V.

12. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>4</sup> in the amino acid sequence of formula (2) is N.

13. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>5</sup> in the amino acid sequence of formula (2) is Q.

14. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>6</sup> in the amino acid sequence of formula (2) is S or T.

15. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>7</sup> in the amino acid sequence of formula (2) is A.

16. The anti-human-norovirus GII antibody according to claim 1, wherein X<sup>8</sup> in the amino acid sequence of formula (2) is M.

17. The anti-human-norovirus GII antibody according to claim 1, wherein the amino acid sequence of formula (2) is selected from the group consisting of:

V-N-Q-F-Y-S-L-A-P-M (2-1)(SEQ ID NO: 13),

V-N-P-F-Y-T-L-A-P-M (2-2) (SEQ ID NO: 14),

V-N-Q-F-Y-T-L-A-P-M (2-3) (SEQ ID NO: 15),

V-N-Q-F-Y-T-L-A-P-V (2-4) (SEQ ID NO: 16),

V-N-Q-F-Y-S-L-A-P-M (2-5) (SEQ ID NO: 17),

G-N-Q-F-Y-T-L-A-P-M (2-6) (SEQ ID NO: 18),

V-N-Q-F-Y-S-L-A-P-V (2-7) (SEQ ID NO: 19), and

V-S-S-F-Y-I-L-S-P-V (2-8) (SEQ ID NO: 20).

\* \* \* \* \*

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : 9,244,072 B2  
APPLICATION NO. : 14/344784  
DATED : January 26, 2016  
INVENTOR(S) : Motohiro Miki

Page 1 of 1

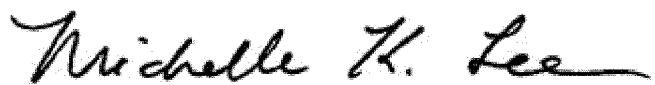
It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

On the title page, Item (86), the PCT information is incorrect. Item (86) should read:

--(86) PCT No.: **PCT/JP2012/073511**

§ 371 (c)(1),  
(2), (4) Date: **Mar. 27, 2014**--

Signed and Sealed this  
Seventeenth Day of May, 2016



Michelle K. Lee  
Director of the United States Patent and Trademark Office